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7, 2005, 20:44:40; Search time 121.533 Seconds (without alignments) 273.682 Million cell updates/sec
                                                                                                                                                                                                                                            1 AVITGACERDVQCGAGTCCA.....CSRFPDGRYRCSMDLKNINF
GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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                                                                              - protein search, using sw model
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Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Post-processing:

Database :

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Aab70146 Human G p Abb76801 Human ZAQ Abj05338 Human ZAQ Aao15529 Human phy Abb06306 Human G p Aae24333 Human pro Add69104 Human ZAQ Human pro Human pro Human pro Membrane-A human T Human G p Amino aci Human ang Human PRO Human PRO Endocrine Human PRO Human PRO Human ext Amino Human Description Add69104 Add69104 Add69104 Add69104 Add691056 Add691056 Add69109 Add69109 Add69109 Add69109 Add69173 Add69173 Add69173 Add69107 SUMMARIES AAU83674 ABB84902 AAO15527 AAE24392 AAY66745 AAU12406 AD005360 **AAB65268** AAB48175 ADN43256 ADR24003 AAB18453 AAB48067 AAB70146 4BB76801 В Query Match Length 100.0 0.001 007 00 8 Score Result Š.

105 5 ABB06308 105 5 AAE24382 105 6 ABB95508 105 6 ABU58083 105 6 ABU58073 105 6 ABU28073 105 6 ABU60821 105 6 ABU60821 105 6 ABU60821 105 6 ABU60800 105 6 ABU60800		Human	Novel		Nove	Human	Human	Novel	Human	Human	Human	Abu07603 Human ZVE	Abu72559 Novel hum	Human	Abu59885 Novel sec	Human B	Abo26005 Human PRO	Abo25075 Human sec
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ALIGNMENTS

RESULT 1

Human; G protein-coupled receptor protein; nootropic; neuroprotective; hypotensive; orexigenic; antiallergic; antianginal; antimicrobial; antibacterial; gene therapy; Alzheimer's disease; hypertension; anorexia; allergy; angina pectoris; infection; MRA; multiple resistant Staphylococcus aureus. Human G protein-coupled receptor protein-related sequence #2. AAB70146 standard; protein; 86 AA 27-AUG-1999; 99JP-00241531. 18-JUL-2000; 2000JP-00217474. 24-AUG-2000; 2000WO-JP005685 (TAKE) TAKEDA CHEM IND LTD WO200116309-A1 Homo sapiens 29-MAY-2001 08-MAR-2001 AAB70146; AAB70146

Terao Y, Shintani Y; Watanabe T,

WPI; 2001-226684/23

New human brain-originated guanosine triphosphate protein-coupled receptor protein, its salt and encoded gene, useful in (gene) diagnosis and development of preventives and remedies for Alzheimer's disease, hypertension and anorexia.

Example 4; Fig 9; 119pp; Japanese.

The present sequence is provided in a specification relating to a protein or its salt with an amino acid sequence identical or substantially similar to a fully defined sequence of 393 amino acids as given in the specification. The protein is useful in gene diagnosis and development of preventives and remedies for diseases associated with dysfunction of the protein, e.g. Alzheimer's disease, hypertension, anorexia, allergy, angina pectoris and infections (e.g. multiple resistant Staphylococcus aureus. The proteins and DNA encoding the proteins are also useful for

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The invention comprises a method of producing a target peptide. The C-terminal end of the target peptide is fulsed via a protease-susceptible linker to parathyroid hormone (PTH) residues 1-34. The method of the invention is useful for the clean and efficient production of a target peptide at a high expression rate on an industrial scale without the need protence the N-terminal methionine from the product. The peptides produced by the method of the invention are suitable for pharmaceutical and other uses. The present protein sequence was used in the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Production of target peptide comprises cleavage of fusion peptide with parathyroid hormone peptide for efficient manufacture of target peptide without the need to remove N-terminal methionine.
                                                                                                                                                                                                                                             Target peptide production; fusion peptide; protease-susceptible linker; parathyroid hormone; PTH; high expression rate;
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100.0%; Pred. No. 7.4e-47;
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                                                                                           standard; protein; 86
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27-JUN-2001; 2001JP-00195522.
                                                                                                                                                                                                                                                                                    pharmaceutical application.
                                                                                                                                                                   08-NOV-2002 (first entry)
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                                                                                                                                                                                                          Human ZAQ protein ligand.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                proteins. The method comprises preparing a recombinant vector for transforming a host cell before culturing the obtained transformant, assaying expression of the reporter gene and confirming high expression of the recombinant proteins are useful as drugs, reagents, raw materials for industries and feeding stuffs. Also, the proteins are obtainable on large-scale production. The present sequence was used to illustrate the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Production of recombinant proteins in prokaryotes or eukaryotes particularly with target proteins obtainable through gene recombination technique, for use as drugs, reagents, raw materials for industries and
                                                                                                                                                                     1 AVITGACERDVQCGAGTCCAISLMLRGLRMCTPLGREGEECHPGSHKVPFFRKKKHHTCP
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100.0%; Pred. No. 7.4e-47;
ive 0; Mismatches 0;
                                                                         Score 498; DB 4;
Pred. No. 7.4e-47;
the treatment of these diseases by gene therapy
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                                                                       100.0%;
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nes 86; Conservative
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use in
                          ZAQ ligand; physiologically-active ZAQ ligand; digestive disease;
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Human physiologically-active ZAQ ligand-related protein 4.
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17-MAY-2001; 2001JP-00147759.
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Best Local Similarity 100.
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                                           colitis; diarrhoea
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                                                                                               WO200257443-A1.
                                                                     Homo sapiens.
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The present invention describes a peptide containing an amino acid sequence (1) identical to or substantially similar to that of the sequences in ABB06305 or ABB06306, or its salt. (1) has antidiarrheic and laxative activities. The peptides and encoding DNAs from the present invention are useful for developing drugs to treat digestive diseases like collitis, diarrhoea, constipation and poor-absorption syndrome, including gene therapy. The physiologically-active cows milk-originated peptides are applicable as a specific ligand of brain-originated orphan G protein-coupled receptor protein ZAQ, ABB49615 to ABB40659 and ABB06303 present invention
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                                                                                                                                   Physiologically-active peptides from cows milk, useful for developing drugs to treat ZAQ-mediated diseases, particularly digestive diseases like colitis, diarrhea, constipation and poor-absorption syndrome, by gene therapy.
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                                                    Takatsu Y,
                                                                                                                                                                                                       Claim 1; Fig 9; 191pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE24383 standard; protein; 86
                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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02-FEB-2001; 2001JP-00026779.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           86; Conservative
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                         (TAKE ) TAKEDA CHEM IND
                                                      Masuda Y,
                                                                                              2002-188546/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ehlert FJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                            N-PSDB; ABL49635
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 86 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                     Hinuma
                                                       Ohtaki
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Bullock CM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO2003088904-A2
                                                                                                                 Sequence 86 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                    ADO05360;
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                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                    RESULT 8
ADO05360
  X8888888888
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                                             gastrointestinal smooth muscle contraction, useful for improving impaired gastrointestinal motility in irritable bowel syndrome, chronic
                                                                                                            The invention relates to human prokineticin 1 and 2 polypeptides that etimulate gastrointestinal smooth muscle contraction and nucleic acid molecules encoding such polypeptides. Polypeptides of the invention are useful for treating disorders involving impaired gastrointestinal motility. They are useful for stimulating gastrointestinal motility in operational ileus, chronic constipation and gastrointestinal reflux disease. The proxinction antagonists are useful for inhibiting gastrointestinal motility in conditions of diarrhoea, malabsorptive disease. The proxineticin antagonists are useful for inhibiting disorders, inflammatory bowel disorders, infectious diseases and intestinal cancers. The antagonists also act as analgesics. The present sequence is human prokineticin 1 mature protein
                                                                                                                                                                                                                                                                                                                                     9
                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Angiogenesis inhibitors for treatment and prevention of cancer, ovarian diseases and inflammatory disease.
                                                                                                                                                                                                                                                                                                                                    1 AVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP
                                                                                                                                                                                                                                                                                                                                                1 AVITGACERDVQCGAGTCCAISLMLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP
                                                                                                                                                                                                                                                                                                             Gaps
                                   New isolated human prokineticin 1 and 2 polypeptides that stimulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      angiogenesis inhibitor; cytostatic; antiinflammatory; cancer; ovarian disease; diabetic retinopathy; inflammatory; ZAQ; Bv8; ISE;
                                                                                                                                                                                                                                                                                                             ;
                                                                                                                                                                                                                                                                                       Length 86;
                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                    100.0%; Score 498; DB 5; ilarity 100.0%; Pred. No. 7.4e-47; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human ZAQ-related protein - SEQ ID 82.
                                                                                                                                                                                                                                                                                                                                                                                               CLPNLLCSRFPDGRYRCSMDLKNINF
                                                                                                                                                                                                                                                                                                                                                                                CLPNLLCSRFPDGRYRCSMDLKNINF
                                                                                          Claim 1; Page 79-80; 86pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADD69104 standard; protein; 86 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Takatsu
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 2002-479752/51.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-646310/61
                                                                                                                                                                                                                                                                                                Local Similarity
les 86; Conserv
           N-PSDB; AAD39321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003066860-A1.
                                                                                                                                                                                                                                                               Sequence 86 AA;
                                                                     constipation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens.
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                                                                                                                                                                                                                                                                                     Query Match
Best Local Si
Matches 86;
                                                                                                                                                                                                                                                                                                                                                                                61
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                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human, prokineticin 1, PK1; circadian rhythm, modulation, drug screening; circadian rhythm disorder; non-24-hour sleep-wake syndrome; rapid time-zone change syndrome; jetlag; work-shift syndrome; delayed phase sleep syndrome; advanced sleep phase syndrome; irregular sleep-wake pattern syndrome; decreased amplitude syndrome; hunger; infardian rhythm; daydreaming; urination; hunger; infardian rhythm; female sexual receptivity; CNS; central nervous syndrome; PK2 receptor ahtagonist.
The invention relates to a novel angiogenesis inhibitor comprising a compound that inhibits the activity of an amino acid sequence given in the specification. Angiogenesis-related proteins BN9, ZAQ and ISE were utilised within the method of the invention. The molecules of the invention demonstrate cytostatic and antiinflammatory activities whilst the method may be useful for treatment and prevention of cancer, ovarian diseases, diabetic retinopathy and inflammatory disease. The current sequence is that of the human ZAQ-related protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AVITGACERDVQCGAGTCCAISLWIRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP
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                                                                                                                                                                                                                                                                                                                                                                                                                                Length
                                                                                                                                                                                                                                                                                                                                                                                                                            Score 498; DB 7;
Pred. No. 7.4e-47;
Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
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nes 86; Conservative
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                                                                                                                                                                                                                                          neurogenesis; prokineticin receptor; PKR; neural stem; progenitor cell; neural regeneration; Alzheimer's disease; Parkinson's disease; neurodegenerative disease; prokineticin 1; PKI.
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                                                                                                                                                                                                                      0; Gaps
                                                                                                                                                                                                         Length 86;
                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                  Amino acid sequence of human prokineticin 1 (PK1).
                                                                                                                                                                                                        100.0%; Score 498; DB 7;
100.0%; Pred. No. 7.4e-47;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                              86
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                                                                                                                                                                                                                                                             61 CLPNLLCSRFPDGRYRCSMDLKNINF
                                                                                                                                                                                                                                                                                                            ADN43256 standard; protein; 86 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                03-OCT-2003; 2003WO-US031626
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les 86; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cheng MY;
                                                                                                                                                                                                                                                                                                                                                                                                       WO2004032851-A2.
                                                                                                                                                                                              Sequence 86 AA;
                                                                                                                                                                                                                                                                                                                                                                                         Homo sapiens
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antiangiogenic; antialcoholic; antiarrhythmic; antiarteriosclerotic;
anticonvulsant; antidepressant; antidiabetic; anti-HIV; antimanic;
antiparkinsonian; cerebroprotective; cytostatic; eating disorders;
antiparkinsonian; cerebroprotective; cytostatic; eating disorders;
andorine; gastrointestinal; gynecologidal; hypnotic; hypotensive;
neuroleptic; neuroprotective; noctropic; ophthalmologidal; tranquilizer;
wasotropic; vulnerary; monoclonal antibódy; human; ZAQL-1; ligand;
wyoulation disorder; digestive disease; andiogenesis; pregnancy;
eating disorder; aleeping disorder; seasonal depression;
reproductive dysfunction; endocrine disease; senile dementia;
w lizheimer's disease; aging; cerebral circulatory disorder; head trauma;
w painal injury; epilepsy; anxiety; depression; schizophrenia; alcoholism;
w premenstrual disorder syndrome; glaucoma; AIDS; diabetes.
                                                                                                                                           The specification describes a method for identifying a compound that modulates neurogenesis. The method comprises providing a compound that modulates prokineticin receptor (PKR) signaling, contacting a neural stem or progenitor cell with the compound, and determining the ability of the compound to modulate neurogenesis. The method is useful for modulating neurogenesis or for identifying compounds that modulate neurogenesis.

These are used for both ex vivo or in vivo therapeutic applications where neural regeneration is desirable, such as in Alzheimer's disease.

Parkinson's disease or other debilitating neurodegenerative diseases. The present sequence represents human prokineticin 1 (PKI), which may be used in the method of the invention to modulate neurogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AVITGACERDVQCGAGICCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AVITGACERDVQCGAGTCCAISLWLRGLRWCTPLGREGEECHPGSHKVPFFRKKKHHTCP 60
          Identifying a compound that modulates neurogenesis comprises contacting neural stem or progenitor cell with a compound that modulates prokineticin receptor signaling and determining its ability to modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 86;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 498; DB 8; 100.0%; Pred. No. 7.4e-47;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLPNLLCSRFPDGRYRCSMDLKNINF
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                                                                                                             Claim 26; Fig 6B; 103pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human ZAQ-1 ligand protein #1.
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Les 86, Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 86 AA;
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                                                                           neurogenesis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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The invention relates to human prokineticin 1 and 2 polypeptides that stimulate gastrointestinal smooth muscle contraction and nucleic acid molecules encoding such polypeptides. Polypeptides of the invention are useful for treating disorders involving impalred gastrointestinal motility. They are useful for stimulating gastrointestinal motility in disorders such as irritable bowel syndrome, diabetic gastroparesis, postoperational ileus, chronic constipation and gastrointestinal reflux disease. The prokineticin antagonists are useful for inhibiting disorders inflammatory bowel disorders, infectious diseases and intestinal cancers. The antagonists also act as analgesics. The present
                                                                                                                                 New isolated human prokineticin 1 and 2 polypeptides that stimulate gastrointestinal smooth muscle contraction, useful for improving impaired gastrointestinal motility in irritable bowel syndrome, chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 AVITGACERDVQCGAGTCCAISLMLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 498; DB 5;
Pred. No. 7.5e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence is human prokineticin 1 mutant protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Scor. 100.0%; Pred. No. 7.55. 100.0%; Pred. No
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Ehlert FJ;
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                                                                                                                                                                                                                                                                                                                                                                        human ZAQL-1 ligand polypeptides, comprising either of two fully defined sequences of 86 amino acids (S1). (I) is ZL1-107 or ZL1-234a produced from hybridoma cells ZL1-107 FERM BP-8256 or ZL1-234 FERM BF-8257. (I) is useful for carrying out assay of the polypeptide containing FERM BF-8257. (I) is involves reacting (I) with the test-liquid containing the polypeptide or its salt, and measuring the ratio of the polypeptide bound to (I). (I) is useful as a diagnostic or therapeutic agent for diagnosts and/or treatment of diseases such as endometrial cancer, endometriosis or ovulation disorders, diseases relating to pregnancy, eating disorder, sleeping disorder, seasonal depression, reproductive dysfunction, endocrine disorder, seasonal depression, reproductive dysfunction, endocrine by aging, cerebral circulatory disorder, head trauma, spinal injury, epilepsy, anxiety, depression, manic depression, schizophrenia,
                                                                                                                                                                                                                                                                                                                                                  The invention relates to a monoclonal antibody (I) having high avidity to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9
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                                                                                                 New monoclonal antibody having high avidity to human ZAQL-1 polypeptide, useful for preventing, treating or diagnosing diseases such as endometrial cancer, ovulation disorders, Alzheimer's disease, AIDS, Parkinson's disease and diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alcoholism, Parkinson's disease, hypertension, arteriosclerosis, arrhythmia, premenstrual disorder syndrome, glaucoma, AIDS, diabetes, etc. This sequence corresponds to a ZAQ-1 ligand used in the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AVITGACERDVOCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP
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                                                                                                                                                                                                                                                                          Claim 1; SEQ ID NO 1; 64pp; Japanese
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   The invention relates to human prokineticin 1 and 2 polypeptides that stimulate gastrointestinal smooth muscle contraction and nucleic acid molecules encoding such polypeptides. Polypeptides of the invention are useful for treating disorders involving impaired gastrointestinal motility. They are useful for stimulating gastrointestinal motility in disorders such as irritable bowel syndrome, diabetic gastroparesis, postoperational ileus, chronic constipation and gastrointestinal reflux disease. The prokineticin antagonists are useful for inhibiting gastrointestinal motility in conditions of diarrhoes, malabsorptive disorders, inflammatory bowel disorders, infectious diseases and intestinal cancers. The antagonists also act as analgesics. The present sequence is human prokineticin 1 mutant protein
gastrointestinal smooth muscle contraction, useful for improving impaired gastrointestinal motility in irritable bowel syndrome, chronic constipation.
                                                                                                                                                                                                                                                                                    Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand; pharmaceutical; receptor immunoadhesin; gene mapping.
                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                                                                                                                                                         Query Match
100.0%; Score 498; DB 5; Length 89;
Best Local Similarity 100.0%; Pred. No. 7.7e-47;
Matches 86; Conservative 0; Mismatches 0; Indels
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                                                 Example 1; Page 84; 86pp; English.
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98US - 0087609P.
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us-10-811-328-3.rag

Sequence 105 AA;

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The invention provides membrane-bound PRO polypeptides and polynucleotides encoding them. The PRO sequences of the invention were identified based on extracellular domain homology screening. The PRO sequences have homology with proteins including LDL receptors, TIE ligands and various enzymes. The membrane-bound proteins and receptor molecules are useful as pharmaceutical and diagnostic agents. Receptor immunoadhesins, for instance, can be used as therapeutic agents to block receptor-ligand interactions. The membrane-bound proteins can also be employed for screening of potential peptide or small molecule inhibitors of the relevant receptor/ligand interaction. The PRO encoding sequences are useful as hybridization probes, in chromosome and gene mapping and in the generation of antisense RNA and DNA. PRO nucleic acid sequences will also be useful for the preparation of PRO polypeptides, especially by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Membrane-bound proteins and related nucleotide sequences.
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98US - 0094651P .
98US - 009528EP .
98US - 009530EP .
98US - 0095301P .
98US - 0095318P .
98US - 0095321P .
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (GETH ) GENENTECH INC.
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Yuan J;
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                                 04-AUG-1998;
04-AUG-1998;
04-AUG-1998;
04-AUG-1998;
04-AUG-1998;
10-AUG-1998;
10-AUG-1998;
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17-AUG-1998;
17-AUG-1998;
17-AUG-1998;
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17-AUG-1998;
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18-AUG-1998;
18-AUG-1998;
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19-AUG-1998;
20-AUG-1998;
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17-AUG-1998;
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17-AUG-1998
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                                                                                                                                    11-AUG-1
11-AUG-1
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Watanabe CK;

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                                                                                                                                                                                                                                                                                                                                                                                                                                            hematopoietic associated disease; atelectasis; pulmonary congestion; oedema; emphysema; chronic bronchitis; bronchial asthma; bronchiectasis; intestinal disorder; spleen associated disease; renal disorder; cardiovascular disorder; ischemic heart disease; hydrocephalus; brain hernitation; latrogenic disease; inflammation; meningitis; Alzheimer's Disease; cerebral toxoplasmosis; Parkinson's disease; multiple sclerosis; hydrocephalus; encephalitis; hepatic disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel human and murine secreted proteins designated TANGO 216, 261, 262, 266 and 267 useful as modulating agents of cellular processes, e.g. for
                                                                   1 AVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP
                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                              TANGO 266; TANGO 216; TANGO 261; TANGO 262; TANGO 267; cellular proliferation; cellular differentiation; cellular adhesion; von Willebrand factor-associated disorder; cell trafficking; cancer;
                                     ö
 Length 105;
                                     Indels
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 100.0%; Score 498; DB 3; 100.0%; Pred. No. 9.1e-47;
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                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          l. .19
/note= "signal sequence"
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                                                                                                                                                           80 CLPNLLCSRFPDGRYRCSMDLKNINF 105
                                                                                                                                      96
                                                                                                                                      61 CLPNLLCSRFPDGRYRCSMDLKNINF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                           AAB18453 standard; protein; 105 AA
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                                                                                                                                                                                                                                                                                                                                                                human TANGO 266 polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-MAR-2000; 2000WO-US005226.
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                                     86; Conservative
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Query Match
Best Local Similarity
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AAB18453
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cancer, modulate the proliferation, differentiation, and/or function of cells that appear in the bone marrow, and leukocytes, treat bone marrow, blood and hematopoietic associated diseases and disorders, atelectasis, pulmonary congestion or oedema, emphysema, chronic bronchitis, bronchial asthma and bronchiectasis, intestinal disorders, spleen associated diseases, modulate renal disorders, treat cardiovascular disorders such as ischemic heart disease, modulate the proliferation, differentiation, and/or function of bone and cartilage cells and to treat bone and/or cartilage associated diseases or disorder. They may also be used to treat disorders associated with the ovaries, cerebral oedema, hydrocephalus, brain herniations, iatrogenic disease, inflammations, bacterial and viral meningitis, Alzheimer's Disease, cerebral toxoplasmosis, Parkinson's encephalitis, and treat hepatic disorders
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 105 AA;
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AVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP 79 1 AVITGACERDVOCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP Gaps ö Length 105; Indels 100.0%; Score 498; DB 3; 100.0%; Pred. No. 9.1e-47; 0; Mismatches CLPNLLCSRFPDGRYRCSMDLKNINF 105 86 CLPNLLCSRFPDGRYRCSMDLKNINF Best Local Similarity 100. Matches 86; Conservative 61 Ouery Match ò 용 8

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Human G protein-coupled receptor protein-related sequence #4. AAB70148 standard; protein; 105 (first entry) 29-MAY-2001 AAB70148; AAB70148 RESULT

Human, G protein-coupled receptor protein, nootropic, neuroprotective, hypotensive, orexigenic, antiallergic, antianginal, antimicrobial, antibacterial, gene therapy, Alzheimer's disease, hypertension, anorexia, allergy, angina pectoris, infection, MRSA, multiple resistant Staphylococcus aureus.

WO200116309-A1. Homo sapiens

08-MAR-2001

24-AUG-2000; 2000WO-JP005685 99JP-00241531 27-AUG-1999;

18-JUL-2000; 2000JP-00217474

(TAKE) TAKEDA CHEM IND LID

Shintani Y; Terao Y, Watanabe T,

WPI; 2001-226684/23.

New human brain-originated guanosine triphosphate protein-coupled receptor protein, its salt and encoded gene, useful in (gene) diagnosis and development of preventives and remedies for Alzheimer's disease, anorexia. hypertension and

Example 4; Page 113; 119pp; Japanese.

The present sequence represents a human Zven2 polypeptide. The specification also describes Zven1. The Zven1 gene is present on chromosome 3p21.1-3p14.3. The specification also describes Zven2 zen polynuclectides and polypeptides are useful in veterinary and human therapeutics, for treating small cell cancer of the lung, to promote wound healing, to prevent or to treat an adverse reaction of the skin to a skin-sensitizing agent or a skin-irritating agent, to stimulate the immunos system of an immunocompromised individual, as antitumour agents, as antiinflammatory agents, as agents to regulate regeneration or

Novel isolated Zven polypeptide useful for inhibiting proliferation of

tumor cells, for treating small cell cancer of lung, to healing, and for treating Crohn's disease and diarrhea.

Claim 27; Page 4; 98pp; English.

to promote wound

The present sequence is provided in a specification relating to a protein or its salt with an amino acid sequence identical or substantially similar to a fully defined sequence of 393 amino acids as given in the

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                                                                                                                                                                                                                                                                                                                                                                                                                       Zvenl; 3p21.1; 3p14.3; Zven2; small cell lung cancer; wound healing; antitumour; antiinflammatory; necrosis; tissue growth; digestive enzyme; cellular differentiation; gastrointestinal cell contractility; gastrointestinal motility; diarrhoea;
specification. The protein is useful in gene diagnosis and development of preventives and remedies for diseases associated with dysfunction of the protein, e.g. Alzheimer's disease, hypertension, anorexis, allergy, angina pectoris and infections (e.g. multiple resistant Staphylococcus aureus. The proteins and DNA encoding the proteins are also useful for the treatment of these diseases by gene therapy
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                                                                                                                                                                                    20 AVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGBECHPGSHKVPFFKKKKHHTCP 79
                                                                                                                                                                    1 AVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP
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                                                                                                                   Length 105;
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                                                                                                                   100.0%; Score 498; DB 4;
100.0%; Pred. No. 9.1e-47;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                          61 CLPNLLCSRFPDGRYRCSMDLKNINF 86
                                                                                                                                                                                                                                                                                                                     AAB68427 standard; protein; 105 AA
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25-FEB-2000; 2000US-00511879.
19-APR-2000; 2000US-00552203.
07-JUN-2000; 2000US-0210332P.
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                                                                                                                                                 86; Conservative
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                                                                                                                                  Local Similarity
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                                                                                             Sequence 105 AA;
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Best Local S
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               cellular
remodeling of tissue, as agents to modulate necrosis or tissue growth developmental arrest, to inhibit proliferation of tumour cells, cellular differentiation and necrosis, to treat disorders associated with gastrointestinal cell contractility, secretion of digestive enzymes and acids, gastrointestinal motility, recruitment of digestive enzymes inflammation, and conditions associated with hypermotility such as diarrhoea and Crohn's disease
                                                                                                                                                                                              20 AVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP
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                                                                                                                           100.0%; Score 498; DB 4; Length 105; 100.0%; Pred. No. 9.1e-47; ive 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                  Human PRO1186 polypeptide sequence.
                                                                                                                                                                                                                                                                                                                      AAU12406 standard; protein; 105 AA
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2000WO-US005004
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99US-0170262P
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99WO-US028551
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                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                      Local Similarity 100.
Les 86; Conservative
                                                                                                     Sequence 105 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200140466-A2.
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02-MAR-2000;
03-MAR-2000;
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20-DEC-1999;
20-DEC-1999;
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18-FEB-2000;
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Matches
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AAU1212-AAU12446 represent novel human secretory and transmembrane PRO polypeptides. The PRO polypeptides are useful to detect other PRO polypeptides, to link bioactive molecules to cells expressing PRO polypeptides, to modulate biological activities of cells expressing PRO polypeptides, and to detect the presence of mammalian lung, colon, polypeptides, and to detect the presence of mammalian lung, colon, polypeptide expression in a cell sample to that in a control sample. Some of the 275 sequences are also useful to etimulate the release of tumour necrosis factor-alpha (TNF-alpha) from human blood, the proliferation or differentiation of chondrocytes, the proliferation or gene expression in proliferation of inner ear utricular supporting cells or of T-proliferation of inner ear utricular supporting cells or of T-proliferation of endothelial cells. Some of the PRO polypeptides may modulate glucose or free fatty acid uptake by skeletal muscle cells or by adipocytes, or inhibit binding of A-peptide to factor VIIA. The PRO polypeptides can be used in assays to identify molecules involved in binding interactions. The polymoleotides encoding PRO polypeptides can be used to generate probes, antisense RNA/DNA, transgenic or knock out animals and can be used in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                              Isolated , secretory and transmembrane PRO polypeptide used to detect other PRO polypeptides, link bioactive molecules to cells expressing PRO polypeptides, and detect the presence of mammalian tumors e.g. lung,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           79
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                                                                                                          28-JUL-2000; 2000WO-US020710.
11-AUG-2000; 2000WO-US022031.
23-AUG-2000; 2000WO-US02352.
24-AUG-2000; 2000WO-US023328.
08-NOV-2000; 2000WO-US030952.
            17-MAY-2000; 2000WO-US013705.
22-MAY-2000; 2000WO-US014042.
30-MAY-2000; 2000WO-US014941.
02-UTN-2000; 2000WO-US015284.
05-UNN-2000; 2000US-0209832P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         breast, prostate, cervical.
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                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC.
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N-PSDB; AAS21478.
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Human; anglogenesis-associated protein; PRO; endothelial cell growth; cardiac hypertrophy; cardiovascular disorder; endothelial disorder; anglogenic disorder; atherosclerosis; osteoporosis; hypertenation; myocardial infarction; diabetic retinopathy; rheumatoid arthritis; Crohn's disease; psoriasis; endometriosis; ulcer; wound healing; cancer; Alzheimer's disease; Huntington's disease; stroke; drug screening; gene therapy; transgenic animal.
Human angiogenesis-associated protein PRO1186, SEQ ID NO:165.
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99US-0123957P 99US-0144758P 99WO-US028313 99WO-US028409 99WO-US012252 99US-0141037P 99WO-US023089 05-JAN-2000; 2000WO-US000219 99WO-US005028 99WO-US021090 99WO-US028565 99WO-US020111 99WO-US020594 99WO-US021547 99WO-US028564 WO200053753-A2 Homo sapiens 20-JUL-1999; 26-JUL-1999; 1999 01-SEP-1999 666 02-DEC-1999 02-DEC-1999 08-MAR-1999 15-SEP-1999 30-NOV-1999 30-NOV-1999 14-SEP-2000 12-MAR-1999 23-JUN-1999 OCT-1 15-SEP-1 08-SEP-1

Goddard A; ark MR, Marsters SA; Mark MR, Ma. M, Wood WI; , Kuo SS, Ma Williams PM, CP, Ferrara N, Gerber H,
AL, Hillan KJ, Kuo SS, M
Watanabe CK, Williams PM, Baker KP, (GETH) GENENTECH INC. Gurney Paoni NF, Pitti RM, Ashkenazi AJ, Sodowski PJ

WPI; 2001-090793/10. N-PSDB; AAC97496.

analyzing or angiogenic New isolated nucleic acid for producing a PRO polypeptide, genetic disorders and treating cardiovascular, endothelial disorders, such as atherosclerosis, wounds or cancer.

Claim 69; Fig 66; 293pp; English.

The invention relates to novel human angiogenesis-associated proteins designated PRO proteins (AABS3064-BS3097), and to nucleic acids encoding to the proteins. The invention also relates to vectors and host cells comprising a PRO nucleic acid, the recombinant production of a PRO protein, PRO antibodies specific for a PRO protein, fusion proteins compounds which inhibit the expression of a PRO gene. The invention additionally encompasses methods of identifying modulators of PRO capression or activity; diagnosing a cardiovascular, endothelial or angiogenic disorder, or a susceptibility to such a disorder by detecting mutations in a PRO gene, or the expression level of a PRO gene within a cardiovascular tissue; treating a cardiovascular, endothelial or particular tissue; treating a cardiovascular, endothelial or angiogenic disorder via the administration of a PRO protein, PRO nucleic acid; and methods of inhibiting or stimulating endothelial cell growth, cardiac hypertrophy or PRO-induced angiogenesis via the administration of a PRO protein, or an agonist or antagonist thereof. PRO cucleic acids, and methods of inhibiting or stimulating endothelial cells, PRO proteins, antibodies adjainst PRO proteins, proceeding administration of a PRO protein, or an agonist or antagonist thereof. PRO cucleic acids, PRO proteins, antibodies adjainst PRO proteins, proceeding athereof adjabetic retinopathy, rheumatoid arthritis, Crohn's disease, Huntington's endometriosis, ulcers, Alzheimer's disease, Huntington's

Eaton DL;

Botstein D, Desnoyers L,

Ashkenazi AJ, Baker KP,

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disease, or stroke. PRO nucleic acids are additionally useful in the recombinant production of PRO proteins, as hybridisation probes to screen libraries to isolate cDNAs with sequence identity to PRO proteins, to map genes encoding PRO proteins, to analyse genetic disorders, and in gene therapy. PRO nucleic acids can also be used to produce transgenic animals useful for the development and screening of potential therapeutic agents. The present sequence represents a PRO protein of the invention
                                                                                                                                                                       transmembrane protein; PRO; cytostatic; cell death; mapping; gene mapping; tissue typing;
                                                                                                                                                             1 AVITGACERDVOCGAGICCAISLWLRGLRMCTPLGREGEBCHPGSHKVPFFRKRKHHICP
                                                                                                                                       Gaps
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                                                                                                               Length 105;
                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                           Human PRO1186 (UNQ600) protein sequence SEQ ID NO:371.
                                                                                                               100.0%; Score 498; DB 4;
100.0%; Pred. No. 9.1e-47;
ive 0; Mismatches 0;
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                                                                                                                                                                                                           86
                                                                                                                                                                                                                        CLPNLLCSRFPDGRYRCSMDLKNINF
                                                                                                                                                                                                           CLPNLLCSRFPDGRYRCSMDLKNINF
                                                                                                                                                                                                                                                                                          AAB65268 standard; protein; 105 AA
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99US-0143048P.
99US-0144758P.
99US-0145698P.
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99US-0149396P.
99WO-US021090.
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99US-0158663P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99WO-US028301
                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                        86; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                    Human; secreted and
                                                                                                                                                                                                                                                                                                                                                                                                chromosomal
                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         diagnostic assay
                                                                                            Sequence 105 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200073454-A1.
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15-SEP-1999;
08-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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17-AUG-1999;
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                                                                                                                  Query Match
Best Local &
                                                                                                                                                                                                                                                                                                                  AAB65268;
                                                                                                                                                                                                                                                                                                                                                                                                 cancer;
                                                                                                                                           Matches
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us-10-811-328-3.rag

WO200075327-A1

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proteins. The PRO proteins have cytostatic activity. The PRO proteins can addolabels or antibodies, that cause cell death. PRO proteins can addolabels or antibodies, that cause cell death. PRO molectide sequences, and their fragments can be used as hybridisation probes, in chromosomal and gene mapping, and in the generation of anti-sense RNA and DNA. They may also be used to produce transgenic animals which are used to develop and screen therapeutically useful reagents. The PRO mucleotide and protein sequence can be used for tissue typing and in treating cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to AAF44470 represent PCR primers and hybridisation probes used in the isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to AAB65300 represent human PRO polynucleotide and protein sequences given in the exemplification of the present invention
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                                                                                                                         PRO polynuclectides used to produce polypeptides used to target bioactive molecules such as toxins, radiolabels or antibodies, to specific cells, to cause targeted cell death.
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Godowski PJ;
Paoni NF;
Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AVITGACERDVOCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP
                                                                                                                                                                                                                                 The present invention describes human secreted and transmembrane PRO proteins. The PRO proteins have cytostatic activity. The PRO proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRO1186; PRO184; neoplastic; cell growth; tumour; cancer; breast; ovarian; renal; colorectal; uterine; prostate; lung; melanoma; central nervous system; leukemia; antitumor; cytostatic.
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/note= "tyrosine kinase phosphorylation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Score 498; DB 4; Length 105; 100.0%; Pred. No. 9.1e-47; ive 0; Mismatches 0; Indels (
Goddard A,
MA, Pan J,
Williams PM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "N-myristoylation site"
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:e= "N-myristoylation site"
Gerber H, Gerritsen ME,
AL, Kljavin IJ, Napier
Tumas D, Watanabe CK,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "N-myristoylation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     'note= "mature protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CLPNLLCSRFPDGRYRCSMDLKNINF
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                                                                                                                                                                                                Claim 12; Fig 266; 935pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
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/note=
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Ferrara N, Fong S,
Grimaldi CJ, Gurney
Roy MA, Stewart TA,
Zhang Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                WPI; 2001-032160/04
                                                                                                 N-PSDB; AAF44237
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 105 AA;
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The invention provides PRO1186 and PRO184 polypetides that can be used for the inhibition of neoplastic cell growth and for treating tumours. The PRO polypeptides can be expressed by standard recombinant methodology. The PRO polypeptides or their agonists are useful for inhibition of neoplastic cell growth and for treating tumours, cancers such as breast, ovarian, renal, colorectal, uterine, prostate, lung, bladder or central nervous system cancers or melanoma and leukemia. The present sequence represents the human PRO1186 polypeptide (encoding cDNA clone ID: DNA60621-1516)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20 AVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKKKHHTCP
                                                                                                                                                                                                                                                                                           Compositions for inhibiting neoplastic cell growth and treating tumor cancer, comprises novel PRO1186 or PRO184 polypeptides or its agonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunosuppressive; cytostatic; neuroprotective; gastroincestinal;
virucide; antibacterial; anti-HIV; human immunodeficiency virus;
antiinfertility; cerebroprotective; nootropic; antiulcer; antifungal;
anticonvulsant; tranquilizer; neuroleptic; vasotropic; gynecological;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Extracellular signaling molecule; EXCS; anti-inflammatory; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                                                                                                                                                                             Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 105;
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                                                                                                                                                                                                             Watanabe CK,
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100.0%; Pred. No. 9.1e-47;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                          Claim 31; Fig 2; 104pp; English.
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                                                                                                            02-JUN-1999; 99WO-US012252.
26-JUL-1999; 99US-0145698P.
05-JAN-2000; 2000WO-US000219.
                                                                             24-FEB-2000; 2000WO-US004914.
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                                                                                                                                                                                                             Ashkenazi AJ, Hillan KJ,
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Matches 86; Conservative
                                                                                                                                                                            (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                         WPI; 2001-071078/08.
                                                                                                                                                                                                                                                            N-PSDB; AAC84469
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 105 AA;
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                                               14-DEC-2000.
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Endocrine gland-derived vascular endothelial growth factor; EG-VEGF; human; cell proliferation; cell migration; fenestration; cell differentiation; anglogenesis; chemotaxis; endocrine; infertility; fertility; polycystic ovary syndrome; ovarian cyst; cancer; cytostatic; diagnosis; therapy.
The invention provides human extracellular signaling molecules (EXCS) and polynucleotides which identify and encode EXCS. EXCS can be expressed by standard recombinant methodology. The amino acid and nucleic acid sequences of EXCS are useful for diagnosing, treating and preventing infections and gastrointestinal (peptic ulcer, dysphagia, pancreatitis), infections and gastrointestinal (peptic ulcer, dysphagia, pancreatitis), contrological (e.g. epilepsy, ischemic cerebrovascular disease, stroke), reproductive (infertility, ovulatory defects, endometriosis), autoimmune (AIDS), Addison's disease), and cell proliferative disorders including cancers (of the breast, adrenal gland, bone). They may also be used to treat fatal familial insomnia, nutritional and metabolic diseases of the nervous system, myopathies, mental disorders (anxiety, schizophrenia, mood), as well as infections caused by parasites (malaria, leishmania, trypanosoma), viral (adenovirus, coronavirus, flavivirus), bacterial (e.g. pneumococcus, staphylococcus, bacillus), and fungal (aspergillus, blastomyces, dermatophytes) agents. The nucleic acids, polypeptides, antagonists, agonists, pharmaceutical compositions, and antibodies may also be used for treating or preventing disorders associated with increased or decreased expression or activity of EXCS. EXCS or properties in which expression of EXCS may be correlated with the dispasse in which expression or expression of EXCS may be correlated with
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the disease, to determine presence or excess expression of EXCS, to monitor regulation of EXCS levels during therapeutic intervention, to detect the presence of associated disorders, as targets in microarray, to generate hybridization probes, and to detect differences in gene sequences among normal, carrier or affected individuals. Antibodies may also be used in diagnoshing disorders, in monitoring patients being treated with EXCS agonists, antagonists or inhibitors. Sequences AAB48057-B48082 represent the EXCS of the invention
                                                                                                                                                                                                                                                                             New human extracellular signaling nucleic acids and polypeptides useful for diagnosing, treating and preventing infections and gastrointestinal, neurological, reproductive, and autoimmune/inflammatory disorders.
                                                                                                                                                      Bandman O, Baughn MR;
                                                                                                                                                        Lal P, Burford N,
                                                                                                                                                                            Lu DAM, Patterson C;
                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Page 89; 114pp; English.
                          99US-0144270P.
99US-0146700P.
99US-0157508P.
        99US-0134949P
                                                                                                                (INCY-) INCYTE GENOMICS INC
                                                                                                                                                                                                                     WPI; 2001-025021/03.
N-PSDB; AAC84303.
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                                                                                                                                                        Yue H,
      19-MAY-1999;
                                                 30-JUL-1999;
                               15-JUL-1999;
                                                                                                                                                                              Azimzai Y,
                                                                                                                                                        Tang YT,
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'note= "N-myristoylated" /note= "N-myristoylated"

Modified-site Modified-site

Homo sapiens

Peptide Protein Modified-site

Wood WI;

Ferrara N, Watanabe C, (GETH) GENENTECH INC.

WPI; 2002-130882/17.

23-JUN-2000; 2000US-0213637P. 07-SEP-2000; 2000US-0230978P. 01-DEC-2000; 2000WO-US032678.

22-JUN-2001; 2001WO-US020116

WO200200711-A2

03-JAN-2002

note= "N-myristoylated" 20. .105 /label= Mature_protein . .19 /label= Signal_peptide Location/Qualifiers

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                                                                                              20 AVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP 79
                                                                             1 AVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP
                                           0; Gaps
Length 105;
                                         Indels
 100.0%; Score 499; DB 4;
100.0%; Pred. No. 9.1e-47;
iive 0; Mismatches 0;
                                                                                                                                                                             80 CLPNLLCSRFPDGRYRCSMDLKNINF 105
                                                                                                                                                           86
                                                                                                                                                           61 CLPNLLCSRFPDGRYRCSMDLKNINF
                                                                                                                                                                                                                                                                                              AAMS0773 standard; protein; 105 AA
                         Best Local Similarity 100.
Matches 86, Conservative
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Query Match

ઠે a ð Endocrine gland-derived vascular endothelial growth factor.

23-APR-2002 (first entry)

AAM50773;

BXXXXX

RESULT 22 AAM50773

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The present sequence is that of a novel, tissue-restricted, growth and differentiation factor termed endocrine gland-derived vascular conditions factor termed endocrine gland-derived vascular endothelial growth factor (EG-VEGF). The sequence is predicted from the copen reading frame of a cDNA clone (see ABA91567) obtained from the copen reading frame of a cDNA clone (see ABA91567) obtained from and constraint issue library. EG-VEGF induces proliferation, migration and fencetrations in capillary endothelial dells derived from endocrine conducthelial cell types tested. The EG-VEGF precursor has a predicted conducthelial cell types tested. The EG-VEGF precursor has a predicted conduction and is predicted to consist of series of short beta strands with large connecting loops held together by disulfide bonds cresulting in a flat fold with finger-like projections that act as interactive surfaces. 80% Homology and 63% identity is shown to venom creating in a flat fold with finger-like projections that act as interactive surfaces. 80% Homology and 63% identity is shown to venom content or human protein Bv8. EG-VEGF futcleic acids and polypeptides, well as agonists and antagonists, can be used in the treatment of the testicular, cervical, adrenal, placental or prostate tissue. The condition may be polycystic ovary syndrome, cancer, especially ovarian cancer, testicular cancer, prostate cancer or uterine cancer, or ovarian cancer, testicular cancer, prostate cancer or uterine cancer, or ovarian cancer, testicular cancer, prostate cancer or uterine cancer, or ovarian cancer, antagonist to inhibit follicle maturation or ovalation. German for antagonial to inhibit follicle maturation or ovalation.

CC antagonial to inhibit follicle maturation or ovalation. Rethods are claimed for identifying compounds that modulate EG-VEGF activity or ovarian or ovalation of a kinase involved in call proliferation. New endocrine gland-vascular endothelial growth factor (EG-VEGF) polypeptides, agonists and antagonists, useful for regulating fertility, and for treating cancer of the reproductive organs, e.g. ovarian or proliferation or survival, to induce chemotaxis, angiogenesis, or differentiation, or to induce endothelial cell proliferation Claim 12; Fig 2; 133pp; English. Sequence 105 AA; N-PSDB; ABA91567 prostate cancer.

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The invention relates to one hundred and twenty two nucleic acids encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides encode human secreted proteins. The PRO nucleic acids, polypeptides, agonists and antagonists are useful for treating a PRO related disorder. CC The PRO polypeptides are useful for diagnosting tumours, rectal tumour or liver tumour. The PRO polypeptides are useful for stimulating the crimal properties are useful for stimulating the proliferation of or gene expression, in pericyte cells, for stimulating the stimulating the release of tumour necrosis factor-alpha from human blood, cf or stimulating or inhibiting the proliferation of normal human dermal fibroblast cells. The PRO polypeptide may also be used as molecular weight markers and for tissue typing. The PRO nucleic acids have applications in molecular biology, including use as hybridisation probes, and in chromosome and gene mapping. AAU83392-AAU83713 represent human PRO crocking and in chromosome and gene mapping. AAU83392-AAU83713 represent human PRO crocking and in chromosome and gene mapping. AAU83932-AAU83713 represent human PRO crocking and in chromosome and gene mapping.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 AVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive; vulnerary; antiarteriosclerotic; PRO agnosist; PRO antagonist; trauma; gene therapy; cardiovascular disorder; endothelial disorder; cancer; angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension; age-related macular degeneration; arterial restenosis; angina; themustoid arthritis; mycoardial infarction; thrombophlebitis; lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma; wound healing; chromosome mappling; gene mapping.
as lung cancer, colon cancer, breast tumor, prostate tumor, rectal tumor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP
                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 498; DB 5; Length 105; 100.0%; Pred. No. 9.1e-47; ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human PRO1186 protein sequence SEQ ID NO:172.
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                                                Claim 11; Fig 166; 359pp; English.
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28-JUL-2000; 2000WO-US020710.
02-AUG-2000; 2000US-022695P.
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25-JUL-2000; 2000US-0220624P.
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23-AUG-2000; 2000WO-US023522.
24-AUG-2000; 2000WO-US023328.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     86; Conservative
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                                                                                                                                                                                                                                                                                                                                                                     Sequence 105 AA;
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                 or liver tumor
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ABB84902
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                                                                                                                20 AVITGACERDVOCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                    Human; secreted protein; PRO; tumour; lung cancer; colon cancer;
breast cancer; proetate tumour; rectal tumour; liver tumour;
pericyte cell proliferation; chondrocyte cell proliferation;
tumour neorosis factor-alpha.
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                 Length 105;
                                                Indels
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             ; Score 498; DB 5;
; Pred. No. 9.1e-47,
0; Mismatches 0
                                                                                                                                                                    80 CLPNLLCSRFPDGRYRCSMDLKNINF 105
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                                                                                                                                                 61 CLPNLLCSRFPDGRYRCSMDLKNINF
                                                                                                                                                                                                                                                                    AAU83674 standard; protein; 105 AA.
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20-DEC-2000; 2000US-00747259,
20-DEC-2000; 2000WO-US034956,
28-PEB-2001; 2001WO-HEAA-156,
01-MAP-15
               100.08;
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2000US-0220666P.
2000US-0220893P.
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22-MAR-2001; 2001US-00816744.
10-MAY-2001; 2001US-00854208.
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2000US-0253646P
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 Query Match
Best Local Similarity 100..
Best Accas 86; Conservative
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10-NOV-2000; 2
28-NOV-2000; 2
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Gaps

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AAO15527 standard; protein; 105 AA
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PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
FF, Watanabe CK, Williams PM, Wood WI, Ye W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
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100.0%; Pred. No. 9.1e-47;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                        01-MAR-2001; 2001WO-US006666.
09-MAR-2001; 2001US-00806689.
22-MAR-2001; 2001US-00806689.
05-APR-2001; 2001US-00816744.
05-APR-2001; 2001US-00854208.
10-MAY-2001; 2001US-00854208.
25-MAY-2001; 2001US-00866028.
25-MAY-2001; 2001US-00866028.
                                                                                            2000WO-US030873.
2000WO-US032678.
2000US-00747259.
                                                                                                                                                  2000WO-US034956.
2001US-00767609.
2001US-00796498.
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Best Local Similarity 100.
Matches 86; Conservative
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N-PSDB; ABL88157.
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                                        24-OCT-2000;
08-NOV-2000;
08-NOV-2000;
                                                                                                                                                                      22-JAN-2001;
28-FEB-2001;
28-FEB-2001;
                                                                                              10-NOV-2000;
01-DEC-2000;
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                                                                                                                                   20-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               expressing
                                                     Human; ZAQ ligand; physiologically-active ZAQ ligand; digestive disease; colitis; diarrhoea.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Industrial production of physiologically-active ZAQ ligand by express in transformant prokaryote and refolding in redox buffer, for use in preventing or treating digestive diseases e.g. colitis and diarrhea.
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                                 Human physiologically-active ZAQ ligand-related protein 3.
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                                                                                                                                                                                                                                                                                                                      22-JAN-2001; 2001JP-00013027.
17-MAY-2001; 2001JP-00147759.
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(first entry)
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24-OCT-2002
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CLPNLLCSRFDGRYRCSMDLKNINF 86

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09-JUL-2001; 2001WO-US021735.
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         WO200236625-A2
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                                                                                                                                                                                                                     constipation.
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                                10-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB95508;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                          Zhou Q,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                      sequence (I) identical to or substantially similar to that of the sequences in ABB06305 or ABB06306, or its salt. (I) has antidiarrheic and laxative activities. The peptides and encoding DNAs from the present invention are useful for developing drugs to treat digestive diseases like colitis, diarrhoea, constipation and poor-absorption syndrome, including gene therapy. The physiologically-active cows milk-originated peptides are applicable as a specific ligand of brain-originated orphan G protein-coupled receptor protein ZAQ. ABL49615 to ABB40659 and ABB06303 to ABB06315 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        20 AVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP 79
                                                                                                                                                                                             Physiologically-active peptides from cows milk, useful for developing drugs to treat ZAQ-mediated diseases, particularly digestive diseases like colitis, diarrhea, constipation and poor-absorption syndrome, by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AVITGACERDVOCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human, prokineticin 1, gastrointestinal motility, intestinal cancer, irritable bowel syndrome; gastrointestinal reflux disease, diarrhoea, diabetic gastroparesis, chronic constipation; malabsorptive disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                           Takatsu Y, Watanabe T, Terao Y, Shintani Y;
                                                                                                                                                                                                                                                                              The present invention describes a peptide containing an amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
0
                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 498; DB 5; Length 105; 100.0%; Pred. No. 9.1e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     inflammatory bowel disorder; analgesic; infectious disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20. .105
/note= "Mature human prokineticin 1"
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0
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    .19
    /label= Signal_peptide

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAE24382 standard; protein; 105 AA
                                                                                                                                                                                                                                                       Claim 5; Page 61; 191pp; Japanese.
                                           17-JUL-2001; 2001WO-JP006162
                                                                  18-JUL-2000; 2000JP-00217442
                                                                              02-FEB-2001; 2001JP-00026779
                                                                                                    (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   86; Conservative
                                                                                                                          T, Masuda Y,
S;
                                                                                                                                                             2002-188546/24
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
                                                                                                                                                                        N-PSDB, ABL49637.
                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 105 AA;
WO200206483-A1
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                                                                                                                                                                                                                                  therapy
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                     24-JAN-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                  gene
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disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; Fig 1; 86pp; English.
01-NOV-2001; 2001WO-US047969
                                                                    03-NOV-2000; 2000US-0245882P
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                                                                                                                                        (REGC ) UNIV CALIFORNIA
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us-10-811-328-3.rag

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Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                One hundred and eighty seven nucleic acids encoding PRO polypeptides, useful in diagnosis and treatment of cardiovascular (e.g. myocardial infarction), endothelial or angiogenic disorders in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 11; Fig 172; 567pp; English.
                                    28-JUL-2000; 2000WO-US020710.
02-AUG-2000; 2000US-US021555.
17-AUG-2000; 2000US-US021555.
23-AUG-2000; 2000WO-US023328.
24-AUG-2000; 2000WO-US023328.
18-SEP-2000; 2000US-00564610.
18-SEP-2000; 2000US-00664610.
18-SEP-2000; 2000US-00665350.
24-OCT-2000; 2000US-00665350.
24-OCT-2000; 2000US-00709238.
08-NOV-2000; 2000WO-US030952.
10-NOV-2000; 2000WO-US030952.
10-DEC-2000; 2000WO-US030952.
20-DEC-2000; 2000WO-US030952.
20-DEC-2000; 2000WO-US030952.
20-DEC-2000; 2000WO-US030956.
22-JAN-2010; 2001WS-00706498.
28-FEB-2011; 2001WS-00706666.
09-MAR-2001; 2001WS-00808689.
                                                                                                                                                                                                                                                                                                                                        2001WO-US017443.
2001WO-US017800.
2001WO-US019692.
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2001WO-US017092
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2001US-00854208
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GERRITSEN M E.
GODDARD A.
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BAKER K P.
FERRARA N.
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GURNEY A L.
HILLAN K J.
MARSTERS S A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PAON N F.
STEPHAN J F.
WATANABE C K.
WILLIAMS P M.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PAN J.
                                                                                                                                                                                                                                                         22-MAR-2001;
05-APR-2001;
10-MAY-2001;
25-MAY-2001;
25-MAY-2001;
25-MAY-2001;
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(FERR/)
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The present invention provides the protein and coding sequences of human PRO proteins. These are useful for treating or diagnosing a cardiovascular, endothelial or angiogenic disorder, including cardiac hypertrophy, trauma, cancer, age-related macular degeneration, atherosclerosis, hypertension, arrerial restenosis, theumatoid arthritis, angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour

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                                                                                  Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver; horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT; antibody-dependent enzyme mediated prodrug therapy.
                                                                 Gaps
angiogenesis (such as breast carcinoma and liver carcinoma) and healing. The present sequence is a PRO protein of the invention
                                                                 ;
                                              100.0%; Score 498; DB 5; Length 105; 100.0%; Pred. No. 9.1e-47; ive 0; Mismatches 0; Indels
                                                                                                                                      80 CLPNLLCSRFPDGRYRCSMDLKNINF 105
                                                                                                                         61 CLPNLLCSRFPDGRYRCSMDLKNINF 86
                                                                                                                                                                                             ABU58083 standard; protein; 105 AA
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98US-008760P

98US-0087759P

98US-008021P

98US-0088021P

98US-0088028P

98US-0088028P

98US-0088028P

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98US-0088021P

98US-0088117P

98US-0088217P

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98US-0088810P.
98US-0088824P.
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97US-0062250P.
97WO-US020069.
97US-0065186P.
97US-0065311P.
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98US-0078910P.
98US-0083322P.
98US-0084600P.
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                                                                                                                                                                                                                                                      Human PRO polypeptide #115.
                                                                                                                                                                                                                                    14-APR-2003 (first entry)
                                         Query Match
Best Local Similarity 10v..
Best Local Similarity
Local Similarity
Set Conservative
                                                                                                                                                                                                                                                                                                                                   US2003027163-A1.
                               Sequence 105 AA;
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13-NOV-1997;
24-NOV-1997;
25-FEB-1998;
20-MAR-1998;
28-MAY-1998;
02-JUN-1998;
02-JUN-1998;
03-JUN-1998;
04-JUN-1998;
04-JUN-1998;
04-JUN-1998;
04-JUN-1998;
                                                                                                                                                                                                                                                                                                                 Homo sapiens.
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05-NOV-1997
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10 - JUN - 199 11 - JUN - 199 12 - JUN - 199 16 - JUN - 199 16 - JUN - 199 17 - JUN - 199 18 - JUN - 199	19-70N-199 19-70N-199 19-70N-199 22-70N-199 23-70N-199 24-70N-199 24-70N-199 24-70N-199 24-70N-199 24-70N-199 24-70N-199 25-70N-199 25-70N-199 25-70N-199 25-70N-199	

BUS-0096778P BUS-0096773P BUS-0096773P BUS-009680F BUS-0096891P BUS-0096891P BUS-0096894P BUS-0096949P BUS-0096949P BUS-0096960P BUS-0096969F BUS-0096969F BUS-0097022P BUS-0097022P	98US-0097661P. 98US-0097952P. 98US-0097954P. 98US-0097954P. 98US-0097974P. 98US-0097974P. 98US-0097978P. 98US-0097978P. 98US-0097978P. 98US-0097978P. 98US-0097978P. 98US-0098014P. 98US-0098014P. 98US-010085P. 98US-010085P. 98US-010085P. 98US-010085P. 98US-010085P. 98US-010085P. 98US-010085P. 98US-010085P. 99US-0113295.	99US-014176PP 99US-014475PP 99US-014475PP 99US-014522P 99US-014522P 99US-014336PP 99US-01501547 99US-01501547 99US-01501547 99WO-US028131 99WO-US028131 99WO-US028131 99WO-US028634 99WO-US03855 90WO-US0003555 90WO-US0003555 90WO-US0004914 000WO-US004414 000WO-US004414 000WO-US005504 000WO-US005504 000WO-US005504 000WO-US005504 000WO-US005504 000WO-US005504 000WO-US005504 000WO-US005504 000WO-US005504	0WO-US006319 0WO-US00884 0WO-US003937 0WO-US01378 0WO-US01376 0WO-US015264 0WS-02136379 0WO-US022031 0WO-US022031
7-AUG-199 7-AUG-199 7-AUG-199 7-AUG-199 7-AUG-199 8-AUG-199 8-AUG-199 8-AUG-199 8-AUG-199 8-AUG-199	26-AUG-1998, 26-AUG-1998, 26-AUG-1998, 26-AUG-1998, 26-AUG-1998, 26-AUG-1998, 26-AUG-1998, 31-AUG-1999, 31-AU	7-40L-1999 6-40L-1999 6-40L-1999 7-40G-1999 5-SEP-1999 6-DEC-1999	0 - MAR - 200 0 - MAR - 200 0 - MAR - 200 0 - MAR - 200 0 - MAY - 200 2 - MAY - 200 2 - MAY - 200 3 - JUN - 200 3 - JUN - 200 3 - JUN - 200 3 - JUN - 200 4 - AUG - 200 4 - AUG - 200
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Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton I Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, I Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Zhang Z;
                                                                                                                                                                                                                                                                                                             15-SEP-1999; 99W0-US028313.
10-DEC-1999; 99W0-US028313.
11-DEC-1999; 99W0-US028313.
11-DEC-1999; 99W0-US028313.
11-DEC-1999; 99W0-US028634.
11-EEB-2000; 2000W0-US0030911.
22-PEB-2000; 2000W0-US0036414.
22-PEB-2000; 2000W0-US0034414.
24-PEB-2000; 2000W0-US003414.
24-PEB-2000; 2000W0-US003414.
24-PEB-2000; 2000W0-US003414.
24-PEB-2000; 2000W0-US003414.
26-PEB-2000; 2000W0-US003414.
26-PEB-2000; 2000W0-US003414.
26-PEB-2000; 2000W0-US003414.
27-PEB-2000; 2000W0-US003414.
28-PEB-2000; 2000W0-US003419.
29-MAX-2000; 2000W0-US01377.
29-MAX-2000; 2000W0-US01377.
29-MAX-2000; 2000W0-US01377.
21-MAX-2000; 2000W0-US01337.
21-MAX-2000; 2000W0-US013358.
21-MAX-2000; 2000W0-US013358.
21-MAX-2000; 2000W0-US013358.
21-MAX-2000; 2000W0-US013526.
21-MAX-2000; 2000W0-US01352.
23-MAY-2000; 2000W0-US01352.
24-AUG-2000; 2000W0-US01352.
24-AUG-2000; 2000W0-US01358.
29-UUN-2001; 2001W0-US013692.
29-UUN-2001; 2001W0-US013692.
29-UUN-2001; 2001W0-US013635.
       9805-0088142P
9805-0088810P
9805-0088824P
9805-0088828P
9805-0088861P
9805-008861P
9805-0089514P
9805-0089512P
9805-0089513P
9805-0089513P
9805-0089518P
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98US-0089907P.
98US-0089908P.
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98WO-US019437.
98WO-US021141.
98WO-US025108.
99WO-US000106.
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                                                              Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing; cardiac insufficiency disorder; cancer; tumour; immune response; adrenal cortical capillary endothelial growth; c-fos induction; vascular endothelial growth factor inhibition; VEGF inhibition; retinal neurons cell growth inhibitor; T-lymphocytes stimulation; retinal disorder; retinitis pigmentosun; kidney disorder; mammalian kidney mesangial cell proliferation; Berger disease; dermatitis; herpetiformis; Crohn's disease; chondrocyte proliferation; chondrocyte redifferentiation; sports injury; arthritis.
                                              Gaps
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                       Query Match
100.0%; Score 498; DB 6;
Best Local Similarity 100.0%; Pred. No. 9.1e-47;
Matches 86; Conservative 0; Mismatches 0;
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97US-0062280P.
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98US-008132P.
98US-008132P.
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98US-008125P.
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     07-SEP-2000; 2000US-0230978P
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1 DL; Godowski PJ; Paoni NF; 1, Wood WI;

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98US-0088033P
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The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in polypeptides are useful in detecting PRO polypeptides in a sample, in modulating a bioactive molecule to a cell expressing a PRO in modulating at least one biological activity of a cell expressing a PRO colypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insufficiency disorders. PRO154 and PRO136, pRO943, PRO828, PRO826, PRO168 or PRO535, PRO826, PRO819, PRO126, PRO1360 and PRO1387 induce c-fos in endothelial growth, and are thus useful for treating canditions or disorders where angiogenesis would be beneficial, e.g. wound healing and antagonist of this polypeptide are useful for treating cancerous tumours. PRO812 inhibits vascular cells useful for treating cancerous tumours. PRO812 inhibits vascular cells and is thus useful for inhibiting endothelial growth. PRO826, PRO1068, PRO1144, PRO1346 and PRO1375 stimulated proliferation of stimulated T-lymphocytes and are therapeutically useful for enhancing immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival/proliferation of thotoreceptor cells) and therefore are useful for treating retinal disorders of injuries, e.g. retinitis pigmentosum, AMD. PRO819, PRO813, and PRO1106 induce proliferation of mammalian kidney meangial cells, and therefore are useful for treating kidney disorders associated with decreased mesangial cell function auch as Berger disease or other ceptroliferation and/or redifferentiation of chondrocytes in culture and are thus useful for treating sports injuries, and arthritis. This is the amino acid sequence of a novel human PRO protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 AVITGACERDVQCGAGTCCAISLMLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP 79
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                                       Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346 and PRO1375, which stimulate proliferation of stimulated T-lymphocytes are therapeutically useful for enhancing immune response and in cancer
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                                                                                                               Claim 12; Fig 266; 648pp; English
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WPI; 2003-247083/24.
               N-PSDB; ABX80360.
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                                                                                     treatments.
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Human, secreted and transmembrane protein; PRO; antiinflammatory; antiarteriosclerotic; cardiant; anti-infertility; anti-HIV; cytostatic; antidiabetic; gene therapy; tumour necrosis factor (TMP)-alpha release; two profession necrosis factor (TMP)-alpha release; two profession modulator; proteoglycan release; cytokine release; tumour; inflammatory disease; organ failure; atherosclerosis; acquired impunodeficiency syndrome; cancer; premature aging; AIDS; acquired immunodeficiency syndrome; cancer; diabetic complication; bioreactor; tissue typing; pharmaceutical; diagnostic; biosensor; bioreactor; tissue typing.
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02-MAR-2000; 2000WO-US005641.
10-MAR-2000; 2000WO-US005841.
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15-MAY-2000; 2000WO-US01376.
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32-MAY-2000; 2000WO-US014941.
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06-JAN-2000; 2000WO-US000376.
11-FEB-2000; 2000WO-US003565.
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             US2003032156-A1
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06-JAN-2000;
06-JAN-2000;
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18-FEB-2000;
22-FEB-2000;
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20-DEC-1999;
20-DEC-1999;
22-DEC-1999;
30-DEC-1999;
                                           06-MAY-2002;
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01-DEC-1999;
01-DEC-1999;
02-DEC-1999;
02-DEC-1999;
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24-FEB-2000;
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02-MAR-2000;
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15-SEP-1999;
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2000Wo-US032678 2000WS-00747259 2001WS-00796498 2001WS-00796498 2001WS-00806662 2001WS-00806666 2001US-00808689 2001US-00808689 2001US-00854208. 2001US-00854280. 2001US-00860216. 2001US-00874503. 2001US-00882636. 2001US-00886342. 2001WO-US021735 2001US-00908827 2001US-00924419 2000WO-US030952 2000WO-US030873 2001US-00866034 2001WO-US017092 2001US-00866028 2001US-00872035 2001WO-US017800 2001WO-US019692 2001US-00887879 2001WO-US020116 2001WO-US021066 2001US-00927796 2001US-00931836 2001US-00028072 14-MAR-2001; 22-MAR-2001; 05-APR-2001; 10-MAY-2001; 10-MAY-2001; 01-DEC-2000; 20-DEC-2000; 20-DEC-2000; 28-PEB-2001; 01-MAR-2001; 09-MAR-2001; 24-AUG-2000; 08-NOV-2000; 10-NOV-2000; 25-MAY-2001; 25-MAY-2001; 01-JUN-2001; 20-JUN-2001; 21-JUN-2001; 22-JUN-2001; 19-DEC-2001; 05-JUN-2001; 09-JUL-2001; 01-JUN-2001; 14-JUN-2001; 29-JUN-2001; 18-MAY-2001; 25-MAY-2001; 06-AUG-2001; 09-AUG-2001,

(GETH) GENENTECH INC.

3 Gao Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gr Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S; Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;

WPI; 2003-341980/32. N-PSDB; ACD24087.

New secreted and transmembrane PRO nucleic acids, for treating inflammation, organ failure, atherosclerbsis, cardiac injury, infertility, birth defects, premature aging, axquired immunodeficiency syndrome (AIDS), or cancer.

Claim 12; Fig 470; 660pp; English.

The invention describes an isolated mucleic acid (I) comprising, or which has 80 % sequence identity to, or the full-length coding sequence of, one cof 275 muclectide sequences, and which encodes a corresponding polypeptide selected from 275 amino acid sequences, where all sequences polypeptide selected from 275 amino acid sequences, where all sequences are given in the specification. The polypeptide encoded by (I) is used to detect PRO polypeptides, link a bioactive molecule to a cell expressing a PRO polypeptide, modulate a biological activity of a cell, stimulate the release of tumour necrosis factor (TMF) alpha from human blood, modulate the uptake of glucose or free fatty acid by cells, stimulate or inhibit composition or differentiation of cells or gene expression, stimulate the release of proteoglycans, stimulate the release of cytokine from peripheral blood mononuclear cells, inhibit the binding of A-peptide from peripheral blood mononuclear cells, inhibit the binding of A-peptide cof factor vIIA, or detect the presence of tumour in a mammal. The nucleic coid and polypeptide encoded by it, are useful for treating inflammatory diseases, organ failure, atherosclerosis, cardiac injury, infertility, birth defects, premature aging, acquired immunodeficiency syndrome (AIDS), cancer, or diabetic complications. The nucleic acid is useful as hybridisation probes, in chromosome and gene mapping, and in generating antisense RNA or DNA. The polypeptides are useful as pharmaceuticals, child sequence of a novel human secreted and transmembrane PRO polypeptide.

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New transmembrane polypeptides and nucleic acids encoding the polypeptides, useful in gene therapy, in chromosome identification, as chromosome markers, or in generating probes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL; Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, God Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paon Roy MA, Stewart TA, Tumas D, Watanabė CK, Williams PM, Wo
        12-UNN-1998; 98US-008910EP.
16-UNN-1998; 98US-008910EP.
16-UNN-1998; 98US-0089512P.
16-UNN-1998; 98US-0089512P.
17-UNN-1998; 98US-0089512P.
17-UNN-1998; 98US-0089512P.
17-UNN-1998; 98US-0089512P.
17-UNN-1998; 98US-0089512P.
17-UNN-1998; 98US-0089512P.
18-UNN-1998; 98US-0089512P.
18-UNN-1998; 98US-0089512P.
18-UNN-1998; 98US-0089513P.
18-UNN-1998; 98US-0089901P.
18-UNN-1998; 98US-0089901P.
18-UNN-1998; 98US-0089901P.
18-UNN-1998; 98US-0089901P.
16-EEP-1999; 98US-0089901P.
17-EEP-1999; 98US-0089901P.
17-EEP-1999; 98US-0089901P.
17-EEP-1999; 98US-0089901P.
17-EEP-1999; 98US-0089901P.
17-EEP-1999; 98US-0089901P.
17-EEP-1999; 98US-0089901P.
18-UNN-1999; 99WO-US01947.
19-EEP-1999; 99WO-US01947.
19-EEP-2000; 2000WO-US0191.
11-EEB-2000; 2000WO-US0191.
11-EEB-2000; 2000WO-US0191.
11-EEB-2000; 2000WO-US0191.
11-MAX-2000; 2000WO-US0199.
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                                                                                                      1 AVITGACERDVOCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP
                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                               Human; PRO; secreted; transmembrane; signal peptide; pharmaceutical; diagnostic; therapeutic; gene therapy.
                                                                 ;
                                         Length 105;
                                                                 Indels
                                       Match 100.0%; Score 498; DB 6; Local Similarity 100.0%; Pred. No. 9.1e-47; es 86; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                        Human secreted/transmembrane protein, #151.
                                                                                                                                                             CLPNLLCSRFPDGRYRCSMDLKNINF 105
                                                                                                                                               98
                                                                                                                                              CLPNLLCSRFPDGRYRCSMDLKNINF
                                                                                                                                                                                                                                           ABU60592 standard; protein; 105 AA
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9710S-0062250P.
9710S-0065211P.
9710S-0065311P.
9710S-0065311P.
9710S-0065311P.
9810S-0078910P.
9810S-0083122P.
9810S-0087128P.
9810S-0087128P.
9810S-0087128P.
9810S-0088021P.
9810S-00880228P.
9810S-0088028P.
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                                                                                                                                                                                                                                                                                               01-MAY-2003 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                     US2002160384-A1.
                 Sequence 105 AA;
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12-NOV-1997;
13-NOV-1997;
24-NOV-1997;
26-FEB-1998;
26-APR-1998;
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28-MAY-1998;
02-JUN-1998;
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02-JUN-1998;
03-JUN-1998;
04-JUN-1998;
04-JUN-1998;
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05-JUN-1998;
05-JUN-1998;
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                                                                                                                                                                                                                                                                     ABU60592;
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                                           Query Match
                                                         Best Loc
Matches
                                                                                                                                                                                                                   RESULT 33
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Ε,

Paoni NF; Wood WI; Godowski

Gaps ;

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The present invention relates to the isolation of novel human PRO polypeptides, and the polynucleotide sequences encoding them. The PRO polypeptides are secreted and transmembrane proteins. The PRO polypeptides and polynucleotides are useful for preparing a medicament useful in the diagnosis and treatment of tumours. Anti-PRO antibodies are useful in diagnostic assays for PRO, by detecting its expression in specific cells, tissues or serum, and for affainty purification of PRO from recombinant cell culture or natural sources. ABUS0139-ABUS0860 represent the human PRO polypeptides of the invention. Note: The sequence data for this patent was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New genes, and its encoded secreted and transmembrane polypeptides, useful for stimulating Tumor Necrosis Factor alpha, or chondrocyte or pericyte proliferation, especially for treating lung tumors, arthritis or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20 AVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiarthritic; osteopathic; gene therapy; TNF-Agonist-Alpha; chondrocyte stimulator; pericyte stimulator; fibroblast modulator; pharmaceutical; diagnostic; biosensor; bioreactor; tumour; lung tumour; colon tumour; breast tumour; prostate tumour; rectal tumour; liver tumour; bone disorder; cartilage disorder; sports injury;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gerritsen ME, Goddard A, Godowski PJ;
Smith V, Stephan JF, Watanabe CK, Wood WI;
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                                                                                                                                                                                                                                                                                                                                                                                                            Length 105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel human secreted and transmembrane protein PRO1186.
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                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 498; DB 6;
100.0%; Pred. No. 9.1e-47;
iive 0; Mismatches 0;
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Claim 11; Fig 166; 314pp; English.
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29-JUN-2001; 2001MO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.
Best Local Similarity 100.
Matches 86; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (GETH ) GENENTECH INC
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N-PSDB; ACD68675.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      arthritis; wound
                                                                                                                                                                                                                                                                                                                                                          Sequence 105 AA;
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Grimaldi JC,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The invention discioles isolated rate secretes, transmendants polypeptices comparising a sequence without signal peptide and the nucleic acid encoding them. The polypeptides can be used to raise antibodies that specifically bind to the PRO polypeptide, for linking a bioactive molecule to a cell expressing a PRO protein and for modulating at least one biological activity of a cell. The PRO polypeptides or polymouclectides are also useful in gene therapy, in chromosome cidentification, as chromosome markers, or in generating probes. The PRO polypeptides are useful as molecular markers for protein electrophoresis, and the isolated nucleic acids may be used for recombinantly expressing those markers. The PRO polypeptides are useful in diagnostic assays for issue typing. Anti-PRO antibodies are useful in diagnostic assays for natural sources. The sequences presented in ABU60478-ABU60624 are the PRO polypeptides of the invention of PRO from recombinant cell culture or natural sources. The sequences presented in ABU60478-ABU60624 are the PRO polypeptides are useful in diagnostic assays for natural sources. The sequence data for this patent is also available in electronic format from USPTO at
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; PRO polypeptide; secreted and transmembrane protein; anti-PRO antibody; diagnostic assay; gene expression; tumour; cytostatic.
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                                                  The invention discloses isolated PRO secreted/transmembrane polypeptides
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Smith V, Stephan JF, Watanabe CK, Wood WI;
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100.0%; Score 498; DB 6;
Best Local Similarity 100.0%; Pred. No. 9.1e-47;
Matches 86; Conservative 0; Mismatches 0;
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Claim 12; Fig 266; 650pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seqdata.uspto.gov/sequence.html
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29-JUN-2001; 2001WO-US021066.
09-APR-2002; 2002US-00119480.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (GETH ) GENENTECH INC.
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C, Gurney
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 105 AA;
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RESULT 34 ABU80821

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98US-0089440P 98US-0089512P 98US-0089514P 98US-0089532P 98US-0089538P 98US-0089598P 98US-0089599P 98US-0089600P 98US-0089653P 98US-0089801P 98US-0089907P 98US-0089908P

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06-JAN-2000; 2000WO-US000219
06-JAN-2000; 2000WO-US000376
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18-FEB-2000; 2000WO-US004341
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10-JUN-1998;
10-JUN-1998;
10-JUN-1998;
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04-JUN-1998;
04-JUN-1998;
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The invention describes an isolated nucleic acid molecule comprising a sequence with at least 80% identity to: (a) a nucleotide encoding any of sequence with at least 80% identity to: (a) a nucleotide encoding any of 122 PRO (secreted and transmembrane) polypeptides whose sequences are fully defined in the specification; or (b) any of 122 nucleotide control or the full length coding sequence of any these 122 nucleotide sequences. The PRO polypeptides or polynucleotides are useful concludarly useful for detecting tumours or bloreactors. These are particularly useful for detecting tumours or bloreactors. These are compared to the sequence of any these are compared to the sequence of any these are concludarly useful for detecting tumours, or liver tumour, or time and the sequence of sequences are deferred to the sequence of the sequence of any properties of the sequence of the sequence of the sequence of the sequence of conductory to the sequence of the sequence or archaritis), or wounds. The compared sequence of these diseases and in the diagnostic or determination of the presence of these diseases. The PRO polypeptides are useful in drug screening, particularly as targets of the sequence of these diseases. The PRO polypeptides are useful as molecular weight markers, or for chromosome conting libraries of human on DNA, genomic DNA or mRNA. The PRO genes may also useful as molecular weight markers, or for chromosome content or the sequence of a novel human secreted and content sequence of a novel human secreted and content sequence of a novel human secreted and content contents and sequence of a novel human secreted and contents and sequence of a novel human secreted and contents and
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human, PRO polypeptide, secreted protein, transmembrane protein,
genetic disorder, antibacterial, immunosuppressive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 498; DB 6; Length 105; 100.0%; Pred. No. 9.1e-47; tive 0; Mismatches 0; Indels C
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97US-0062250P.
97US-0065186P.
97US-0065111P.
97US-0067710P.
98US-0075945P.
98US-0078910P.
98US-0084600P.
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Best Local Similarity 100.0
***rhes 86; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 105 AA;
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25-FEB-1998;
20-MAR-1998;
28-APR-1998;
07-MAY-1998;
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98WO-US021141 98WO-US025108

98WO-US01

99WO-US012252

99WO-US028313

2000WO-US022031

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The invention relates to an antibody that binds essentially to the epitope of endocrine gland-derived vascular endothelial growth factors (EG-VECF) and is selected from anti-EG-VECF monoclonal antibodies 1C6, 2A3, 2A8 and 4H9. The composition and methods are useful in regulating cellular proliferation and chemotaxis, e.g in treating conditions associated with hormone-producing tissue such as congenital adrenal hyperplasia, saxual maturation, precocious puberty, McCume-Albright syndrome, hypogonadotropic hypogonadism, ovarian cyst, cancer such as androgen-dependent cancer or infertility. The present sequence represents the amino acid sequence of human endocrine gland-derived vascular
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endocrine gland; vascular endothelial growth factor; ovarian cyst, cellular proliferation; chemotaxis; congenital adrenal hyperplasia; precocious puberty; McCune-Albright syndrome; cancer; infertility;
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                                                                                                                                                                                                                                                                          /note= "N-myristoylated"
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                                                                                                                                                                        l. .19
/note= "Signal peptide"
                                                                                                                                                                                                                                 /note= "Mature EG-VEGF"
                                                                                                                                                  Location/Qualifiers
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2000US-0213637P.
2000US-0230978P.
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2000WO-US032678
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                                                                    androgen-dependent cancer
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N-PSDB; ABX93675.
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                                                                                                                                                                                                                                                    Modified-site
                                                                                                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                                                                                                     Modified-site
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07-SEP-2000;
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                                                                                                            Homo sapiens
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                                                                                                                                                                   Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to the isolation of novel human PRO
polypeptides, and the polynucleotide sequences encoding them. The PRO
polypeptides are secreted and transmembrane proteins. The PRO
polypeptides are secreted and transmembrane proteins. The PRO
polypeptides are secreted and transmembrane proteins. The PRO
polypeptides are useful for detecting other PRO polypeptides, for modulating
biological activities of cells expressing PRO polypeptides, and for linking
chicalitying agonists or antagonists. The polynucleotide sequence
encoding PRO polypeptides are useful as hybridisation probes, in
chromosome and gene mapping, in the generation of antisense RNA and DNA,
in the preparation of PRO polypeptides, for generating transgenic animals
or knockout animals, to construct hybridisation probes for mapping the
gene which encodes the PRO polypeptide, and for the genetic analysis of
individuals with genetic disorders, in gene therapy, for chromosome
identification, as chromosome markers, and for generating probes for PRO
Northern analysis, Southern analysis and Western analysis. ABU13860-
ABU14006 represent the human PRO polypeptides of the invention. Note: The
sequence data for this patent was obtained in electronic format directly
from the USPTO web site at seqdata.uspto.gov/psipsDIBntry.html
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                                                                                                                                                                                                                                                                            DL;
Godowski PJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel secreted and transmembrane polypeptide for modulating biological activity of cell expressing the polypeptide, identifying agonists or antagonists of polypeptide, and as molecular weight markers.
                                                                                                                                                                                                                                                                                                                Paoni NF;
Wood WI;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; EG-VEGF; sexual maturation; hypogonadotropic hypogonadism;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 105;
                                                                                                                                                                                                                                                                          Baker KP, Botstein D, Desnoyers L, Eaton ong S, Gerber H, Gerritsen ME, Goddard A, Gurney AL, Kljavin IJ, Napier MA, Pan J, art TA, Tumas D, Watenabe CK, Williams PM,
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Pred. No. 9.1e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ch 100.0%; Score 498; D
1 Similarity 100.0%; Pred. No. 9.1
86; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 12; Fig 266; 649pp; English.
                                                                                                                                                                                                                                                                                                                                   Tumas D,
                                                                                   28-FEB-2001, 2001WO-US006520.
01-UTN-2001, 2001WO-US017800.
20-UTN-2001, 2001WO-US019692.
25-UTN-2001, 2001WO-US021066.
09-UTL-2001, 2001WO-US0211065.
                             2000WO-US023328.
2000WO-US030952.
                                                                    2000WO-US032678
                                                                                                                                                                                             28-AUG-2001; 2001US-00941992
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                                                                                                                                                                                                                                   (GETH ) GENENTECH LTD.
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N-PSDB; ABX64184.
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                                                                                                                                                                                                                                                                                               Fong S,
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                                                                                                                                                                                                                                                                          Ashkenazi AJ,
Ferrara N, For
Grimaldi JC, (
                         24-AUG-2000;
08-NOV-2000;
                                                                    01-DEC-2000;
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                                                                                                                                                                                                                                                                                                                                       Roy MA,
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ABU08800
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New isolated PRO polypeptide useful for treating diabetes, rheumatoid arthritis, sports injuries, obesity, hearing loss in mammals, stroke, or
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Gerritsen ME, Goddard A, Godowski PJ, Gurney AL, She
Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI,
97US-0069694P.
98US-0072320P.
98US-0074086P.
98US-0074092P.
98US-0077791P.
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06-JAN-2000; 2000WO-US000277.
06-JAN-2000; 2000WO-US00376.
11-FEB-2000; 2000WO-US003565.
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18-FEB-2000; 2000WO-US004342
22-FEB-2000; 2000WO-US004414
24-FEB-2000; 2000WO-US004914
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N-PSDB; ACA67228.
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01-MAR-2000;
 16-DEC-1997;
23-AN-1998;
03-FEB-1998;
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20-MAR-1998;
27-MAR-1998;
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16-DEC-1999;
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08-SEP-1999;
13-SEP-1999;
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29-NOV-1999
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30-NOV-1999
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                                                                                                                                                                                                                                                           Human; PRO polypeptide; secreted and transmembrane protein; anti-PRO antibody; diagnostic assay; gene expression; diabetes; bone disorder; cartilage disorder; rheumatoid arthritis; obssiry; sports injury; osteoarthritis; hyper-insulinaemia; hypo-insulinaemia; hearing loss; coagulation disorder; stroke; heart attack; cardiant; antidiabetic; anorectic; vulnerary; antiarthritic; osteopathic; antirheumatic; auditory; cerebroprotective; angiogenic.
 CLPNLLCSRFDGRYRCSMDLKNINF 86
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                                                                                                                                              ABU81104 standard; protein; 105
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9705-005974P.
9705-0059113P.
9705-0059113P.
9705-0059132P.
9705-0059352P.
9705-0059352P.
9705-0059352P.
9705-0062285P.
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9705-0063735P.
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97US-0069334P
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                                                                                                                                                                                                                                  Human PRO polypeptide #235
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26-AUG-1997;
17-SEP-1997;
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11-DEC-1997;
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Filvaroff E, Ga AL, Sherwood S; ood WI, Zhang Z;

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Sequence 105 AA;
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28-APR-1998;
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                                                                                                                                                                                                                                                                                          1 AVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP 60
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                    Claim 12; Fig 470; 643pp; English
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19-APR-2000; 2000US-0197750P
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hes 86; Conservative
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heart attack
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encodes a Zvenl polypeptide. (I) is useful for inhibiting the proliferation of tumour cells, as probes or primers to clone 5' noncoding regions of a Zven gene, to direct the expression of heterologous gene in tissues of, for example, transgenic animals or patients treated with gene therapy, to detect the expression of a Zvenl or Zvenl gene in biological sample, to detect activated neutrophils, to identify therapeutic or prophylactic agents that medulate the response of a neutrophil to a pathogen, to determine whether a subject's chromosomes contain a mutation in the Zven gene, or to detect aberrations in Zvenl or Zvenl locus. (I) is useful as educational tools, as laboratory practicum kits for courses related to genetics and molecular biology, protein chemistry and antibody production and analysis. The present sequence represents the amino acid sequence of ZVENZ
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100.0%; Pred. No. 9.1e-47;
ive 0; Mismatches 0;
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97US-0062250P.
97WO-US020069.
97US-0065186P.
97US-006511P.
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Matches 86; Conservative
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98US-0088126P.
98US-00881217P.
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98US-0088138P.
98US-008813P.
98US-008818P.
98US-008818P.
98US-008818P.
98US-008910SP.
98US-008910SP.
98US-008910SP.
98US-0089514P.
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2000WO-US006884.
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The invention describes a new isolated nucleic acid molecule comprising the full length coding sequence of the DNA deposited with the American CT Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PTA, 819-PTA, 209439, 201315, etc); or a sequence with at least 80% identity to a DNA cnocding a PRO polypeptide. The PRO polypeptides or polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or bioreactors. These care particularly useful for detecting or treating e.g. malignancies or cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma, leukaemia or lymphoma), hepatitis B, multiple sclerobis, or Crohn's claukaemia or lymphoma), hepatitis B, multiple sclerobis, or Crohn's claukaemia. The PRO polypeptides are useful in drug screening, and in the diagnostic determination of the presence of these diseases. The PRO polypeptides are also useful as molecular weight markers, or for chromosome identification. The PRO genes are useful as hybridisation probes, or for screening libraries of human cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene therapy, particularly for replacing a defective gene. This is the amino acid sequence of a novel thuman secreted and transmembrane PRO polypeptide New genes and secreted and transmembrane polypeptides (e.g. PRO183 or PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's 20 AVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKKKHHTCP 79 Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
Ferrara N, Fong S, Gerber H, Gerriteen ME, Goddard A, Goddoski PJ;
Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J,
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI; 1 AVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP Gaps ö 100.0%; Score 498; DB 6; Length 105; 100.0%; Pred. No. 9.1e-47; ive 0; Mismatches 0; Indels 0 CLPNLLCSRFPDGRYRCSMDLKNINF 86 Claim 12; Fig 266; 663pp; English. 28-AUG-2001; 2001US-00941992. (GETH) GENENTECH INC. WPI; 2003-352829/33. N-PSDB; ACA64406. Sequence 105 AA; Roy MA, Zhang Z; 61 disease 셤 ଚ ઠે

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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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SUMMARIES

	uc	5, Appli	5, Appli	5, Appli	5350, Ap	469	'n	7	2, Appli	7,	714	13,	Н	68	11, Appl	9, Ap	236,	236,	236,	236,	236,	236,	236,		236,	7856,		7858, Ap
	Description	Sequence	Sequence	Sequence	Seguence	Sequence	Sequence	Seguence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Seguence	Seguence	Sednence	Seguence	Sequence	Sequence	Sequence	Sequence	Seguence	Sequence	Seguence	Seguence
SUMMARIES	ID	US-09-712-529-5	US-10-212-201A-5	US-10-212-355-5	US-09-621-976-5350	US-09-513-999C-4698	US-09-712-529-2	US-10-212-201A-2	US-10-212-355-2	US-09-161-241-14	US-09-949-016-7146	US-09-161-241-13	US-09-161-241-12	US-09-949-016-6872	US-09-161-241-11	US-09-161-241-9	US-09-907-794A-236	US-09-905-125A-236	US-09-902-775A-236	US-09-906-700-236	US-09-903-603A-236	US-09-904-920A-236	US-09-909-064-236	US-09-905-381A-236	US-09-906-618-236	US-09-949-016-7856	US-09-949-016-7857	US-09-949-016-7858
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US-09-161-241-8 US-09-161-241-10	US-09-976-594-1086	US-09-467-997-1	US-09-561-709B-13	US-09-949-016-11293	US-08-219-237B-5	US-08-477-347-13	US-08-476-862-4	US-08-468-560C-5	US-08-828-683A-13	US-09-800-909-4	US-09-800-908-13	US-09-523-323-54	US-08-232-087A-9	US-08-974-022-48	US-08-795-445A-48	US-08-795-447A-48
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ALIGNMENTS

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1 AVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP 60
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100.0%; Score 498; DB 4;
Best Local Similarity 100.0%; Pred. No. 3.6e-51;
Matches 86; Conservative 0; Mismatches 0;
                            Sequence 5, Application US/09712529
Patent No. 6485938
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Bishop, Paul D.
APPLICANT: Bishop, Paul D.
APPLICANT: Thompson, Penny P.
APPLICANT: Thompson, Human Zven Proteins
FILE REFRENCE: 99-61
CURRENT APPLICATION NUMBER: US/09/712,529
CURRENT APPLICATION NUMBER: US/09/712,529
CURRENT FILING DATE: 2000-11-14
NUMBER OF SEQ. ID NOS: 7
                                                                                                                                                                                                                                                                                      FastSEQ for Windows Version 3.0
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ORGANISM: Homo sapiens
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LENGTH: 105
RESULT 1
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Db 80 CLPNLLCSRFPDGRYRCSMDLKNINF 105

RESULT 2

US-10-212-201A-5

Sequence 5, Application US/10212201A

Patent No. 6756479

GREEAL No. 6756479

APPLICANT: Sheppard, Paul O. APPLICANT: Sheppard, Paul O. APPLICANT: Sheppard, Paul D. APPLICANT: Sheppard, Paul D. APPLICANT: Whitmore, Theodore E. APPLICANT: Whitmore, Theodore E. APPLICANT: Thompson, Penny P. TITLE OF INVENTION: Human Zven Proteins

FILE REFERENCE: 99-81

CURRENT FILING DATE: 2002-08-02

PRIOR PRING PAULICATION NUMBER: US/10/212,201A

CURRENT FILING DATE: 2000-11-14

NUMBER OF SEQ ID NOS: 7

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LOCATION: -19..-1
NAME/KEY: UNSURE
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US-09-621-976-5350
is Sequence 5350, Application US/09621976
is Sequence 5350, Application US/09621976
j RENERAL INFORMATION:
is APPLICANT: Unmas Milne Edwards, J.B.
APPLICANT: Johert, S.
is APPLICANT: Glordano, J.Y.
if TITLE OF INVENTION: ESTS and Encoded Human Proteins.
if TITLE OF INVENTION: ESTS and Encoded Human Proteins.
if TITLE OF INVENTION: ESTS and Encoded Human Proteins.
if TITLE OF INVENTION: ESTS and Encoded Human Proteins.
if TITLE OF INVENTION: ESTS and Encoded Human Proteins.
if TITLE OF INVENTION: USPSET: 000-07-21
is SOFTHENT APPLICATION NUMBER: US/09/621,976
is SOFTHARE: Patent.pm
is SOFTHARE: Patent.pm
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100.0%; Score 498; DB 4;
Best Local Similarity 100.0%; Pred. No. 3.6e-51;
Matches 86; Conservative 0; Mismatches 0;
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APPLICANT: Bishop, Paul D.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Thompson, Penny P.
ITILE OF INVENTION: Human Zven Proteins
FILE REFERENCE: 99-81
CURRENT APPLICATION NUMBER: US/10/212,355
CURRENT APPLICATION NUMBER: US/10/212,355
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
SSOFTWARE: FastSEQ for Windows Version 3.0
SSOFTWARE: FastSEQ for Windows Version 3.0
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 105
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Patent No. 6828425
GENERAL INFORMATION:
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ORGANISM: Homo sapiens
FEATURE:
                                                                         TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                 ch 58.4%; Score 291; DB 4; Length 108; 1. Similarity 58.4%; Pred. No. 8.3e-27; 45; Conservative. 14; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Sheppard, Paul O.
APPLICANT: Sheppard, Paul D.
APPLICANT: Bishop, Paul D.
APPLICANT: Whitmore Theodore E.
APPLICANT: Thompson, Paul D.
APPLICANT: Thompson, Paul D.
APPLICANT: Thompson, Paul D.
APPLICANT: Whitmore S.
APPLICANT: Thompson, Paul D.
APPLICANT: Thompson, Paul D.
APPLICANTON Human Zven Proteins
FILE REFERENCE: 99-81
CURRENT APPLICATION NUMBER: US/10/212,201A
CURRENT FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application US/10212355
Patent No. 6828425
GENERAL INFORMATION:
APPLICANT: Bheppard, Paul O.
APPLICANT: Bheppard, Paul D.
APPLICANT: Thompson, Penny P.
TITLE OF INVENTION: Human Zven Proteins
FILE REFERENCE: 99-81
CURRENT FILING DATE: 2002-08-02
                       NUMBER OF SEQ ID NOS: 7
SOFWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 108
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SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 2, Application US/10212201A Patent No. 6756479 GENERAL INFORMATION:
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        2000-11-14
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                                                                                                              TYPE: PRT
ORGANISM: Homo sapiens
        CURRENT FILING DATE:
                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 45; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-10-212-201A-2
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US-10-212-355-2
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LENGTH: 108
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CARDERAL INCRMANTION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILTE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CL001307
CURRENT TAPPLICATION NUMBER: US/09/949,016
CURRENT FILING DATE: 2000-04-14
PRIOR APPLICATION NUMBER: 60/241,755
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-10-03
PRIOR FILING DATE: 2000-0-08
PRIOR FILING DATE: 2000-09-08
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                                                                                                             58.4%; Score 291; DB 4; Length 108; 58.4%; Pred. No. 8.3e-27; ive 14; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-09-161-241-14
; Sequence 14, Application US/09161241
; Patent No. 6344541
; GENERAL INFORMATION:
; APPLICANT: Bass, Michael B
; APPLICANT: Meng, Daguang
; TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
; TILE REFERENCE: A-548
; CURRENT APPLICATION UNDHER: US/09/161,241
; CURRENT FILING DATE: 1998-09-25
; NUMBER OF SEQ ID NOS: 78
; SOFTWARE: PATENTIN Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; Sequence 7146, Application US/09949016; Patent No. 6812339; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88 CLPGLACLRISFNRFIC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 CLPNLLCSRFPDGRYRC 77
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35.5%;
                                                                                                                                                                                                         45; Conservative
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Best Local Similarity 35.5
Matches 22; Conservative
, ORGANISM: Homo sapiens
US-10-212-355-2
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Gaps

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Sequence 6812. Application US/09949016
; Sequence 6812.39
; GENERAL INFORMATION:
; APPLICANT: VEWTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF;
; TURENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14,755
; PRIOR APPLICATION NUMBER: 60/241,756
; PRIOR FILING DATE: 2000-10-03
; PRIOR FILING DATE: 2000-0-0-03
; PRIOR FILING DATE: 2000-0-0-03
; PRIOR FILING DATE: 2000-0-0-0-08
; PRIOR FILING DATE: 2000-0-0-0-0-08
; PRIOR FILING DATE: 2000-0-0-0-0-08
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NOS: 2077012
                                                                                                                               7 CERDVQCGAGTCCAISLWLRGLRMCTPLGREGEEC----HPGSHKVPFFRKRKHHTCPCL 62
                                                                                                   7 CERDVQCGAGTCCAISLWLRGLRMCTPLGREGEEC----HPGSHKVPFFRKRKHHTCPCL 62
Query Match 20.5%; Score 102; DB 3; Length 259; Best Local Similarity 31.5%; Pred. No. 0.00037; Matches 23; Conservative 8; Mismatches 30; Indels 12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20.5%; Score 102; DB 4; Length 259; 31.5%; Pred. No. 0.00037; ive 8; Mismatches 30; Indels
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Patent No. 6344541
GENERAL INFORMATION:
APPLICANT: Bass, Michael B
APPLICANT: Rans, John K
APPLICANT: Meng, John K
CURRENT RILING NOVEL DKR POLYPEPTIDES
CURRENT APPLICATION NUMBER: US/09/161,241
CURRENT FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 11
LENGTH: 259
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                                                                                                                                                                                                  63 PNLLCSRFPDGRY 75
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Matches 23; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: PRT
ORGANISM: Human
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                                                                                                                                                                        30; Indels 12;
                                                                                                                     Score 102; DB 4; Length 186;
Pred. No. 0.00026;
8; Mismatches 30; Indels
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20.5%; Score 102; DB 3;
Best Local Similarity 31.5%; Pred. No. 0.00029;
Matches 23; Conservative 8; Mismatches 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Bass, Michael B
APPLICANT: Sullivan, John K
APPLICANT: Theilly Lars E
APPLICANT: Wang, Daguang
TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
FILE REFERENCE: A-548
CURRENT FILING DATE: 1998-09-25
CURRENT FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 13
LENGTH: 207
TYPE: PRT
ORGANISM: Human
US-09-161-241-13
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APPLICANT: Sullivan, John K
APPLICANT: Sullivan, John K
APPLICANT: Harbill, Lars E
APPLICANT: Wang, Daguang
TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
FILE REPRENCE: A-548
CURRENT APPLICATION NUMBER: US/09/161,241
CURRENT FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 12
LENGTH: 259
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Patent No. 6344541
GENERAL INFORMATION:
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Patent No. 6344541
                                                                                                                     Query Match
Best Local Similarity 31.5%;
Matches 23; Conservative
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; LENGTH: 186
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-7146
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; ORGANISM: Human
US-09-161-241-12
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-323-157-3
US-10-331-157-3
US-10-331-192-21
US-10-680-554-5
US-10-713-567-3
US-10-911-328-3
US-10-912-907-3
US-10-912-907-3
US-10-871-152-22
US-10-803-554A-82
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Maximum Match 100%
Listing first 45 summaries
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                                                                                        - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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Maximum DB seq length: 2000000000
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Match Length
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                                                                                          OM protein
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18, Appl 18, Appl 15, Appl 15, Appl 15, Appl 15, Appl 371, App 117, 118, 118, 118, 118, 118, 118, 118, Sequence 371, Sequence 371, Sequence 371, Sequence 371, Sequence Seq Sequence Sequence Sequence 3 Sequence 3 Sequence 3 Sequence US-10-343-095A-117 US-10-016-481-18 US-10-323-157-18 US-10-313-567-18 US-10-811-38-18 US-10-912-907-18 US-10-016-415-724-18 US-10-016-481-15 US-10-713-567-15 US-10-713-567-15 US-10-912-907-15 US-10-912-907-15 US-10-912-90 US-09-989-722-371 US-09-989-723-371 US-09-989-723-371 US-09-989-727-371 US-09-989-731-371 US-09-991-73-371 US-09-991-73-371 US-09-991-163-371 US-09-991-163-371 US-09-990-456-371 US-09-990-456-371 US-09-990-731-371 US-09-98-723-371 US-09-98-731-371 US-09-98-731-371 US-09-98-731-371 US-09-989-731-371 US-09-989-731-371 US-09-989-731-371 US-09-989-731-371 US-09-989-731-371 US-09-989-731-371 US-09-989-731-371 US-09-989-731-371 US-09-989-731-371 1000.00 100.0 100.0

ALIGNMENTS

US-10-016-481-3

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1 AVITGACERDVQCGAGTCCAISLWLRGLRWCTPLGREGEECHPGSHKVPFFRKRKHHTCP
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Sequence 3. Application US/10016481
; Sequence 3. Application US/10016481
; Publication No. US20020115610A1
; GENERAL INFORMATION:
; APPLICANT: Zhou, Qun-Yong
; TITLE OF INVENTION: Prokineticin Polypeptides, Related
; TITLE OF INVENTION: Compositions and Methods
; FILE REFERENCE: P-UC 5016
; CURRENT APPLICATION NUMBER: US/10/016,481
; CURRENT PELLOR DATE: 2001-11-01
; PRIOR FILING DATE: 2001-11-03
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FRSESQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 498; DB 13;
100.0%; Pred. No. 2.6e-45;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLPNLLCSRFPDGRYRCSMDLKNINF 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                       86; Conservative
                                                                                                                                                                                                                                                                                                                                     , TYPE: PRT
, ORGANISM: Homo sapiens
US-10-016-481-3
                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
100.0%; Score 498; DB 14; Length 86;
Best Local Similarity 100.0%; Pred. No. 2.6e-45;
Matches 86; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Zhou, Oun-Yong
APPLICANT: Zhou, Oun-Yong
APPLICANT: Bullock, Clayton M.
TITLE OF INVENTION: Screening and Therapeutic Methods For
TITLE OF INVENTION: Treating Circadian Rhythm Disorders
FILE REFERENCE: P-UC 5773
CURRENT APPLICATION NUMBER: US/10/417,426
CURRENT FILING DATE: 2003-04-15
PRIOR APPLICATION NUMBER: US 60/372,836
PRIOR FILING DATE: 2002-04-15
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 9
LENGTH: 86
                                  Sequence 3, Application US/10323157

Publication No. US20030113867A1

GENERAL INFORMATION:

APPLICANT: Zhou. Qun-Yong

APPLICANT: Ehlert, Frederick

TITLE OF INVENTION: Prokineticin Polypeptides, Related

TITLE OF INVENTION: Prokineticin and Methods

FILE REFERENCE: P-UC 5016

CURRENT APPLICATION NUMBER: US/10/016,481

PRIOR FILING DATE: 2002-12-18

PRIOR PLING DATE: 2001-11-01

PRIOR PLING DATE: 2001-11-01

PRIOR FILING DATE: 2001-11-03

NUMBER OF SEQ ID NOS: 19

SOFTWARE: PastSEQ for Windows Version 4.0

SEQ ID NO 3

LENGTH: 86
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 9, Application US/10417426 Publication No. US20030235535A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 100.
Matches 86; Conservative
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ORGANISM: Homo sapiens
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RESULT 2
US-10-323-157-3
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GENERAL INFUGRATION:
GENERAL INFUGRATION:
APPLICANT: MASUDA, Yasushi
APPLICANT: MASUDA, Yasushi
APPLICANT: MASUDA, Yasushi
APPLICANT: TARATSU, Yoshihiro
APPLICANT: TERAO, Yasuko
APPLICANT: TERAO, Yasuko
APPLICANT: HINUMA, Syuji
APPLICANTON NUMBER: US/10/333,192
CURRENT FILING DATE: 2003-01-16
FRIOR FILING DATE: 2000-07-18
FRIOR PILING DATE: 2000-07-18
FRIOR FILING DATE: 2001-02-02
FRIOR APPLICATION NUMBER: PCT/JP01/06162
FRIOR APPLICATION NUMBER: PCT/JP01/06162 9 9 1 AVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEBCHPGSHKVPFFKKRKHHTCP 60 9 1 AVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP 1 AVITGACERDVOCGAGTCCAISLMIRGIRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP 1 AVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP Gaps Gaps ; 0 ö Query Match 100.0%; Score 498; DB 16; Length 86; Best Local Similarity 100.0%; Pred. No. 2.6e-45; Matches 86; Conservative 0; Mismatches 0; Indels Length 86; Indels APPLICANT: Zhou, Qun-Yong
APPLICANT: Zhou, Qun-Yong
APPLICANT: Cheng, Michelle Y.
TITLE OF INVENTION: Screening and Therapeutic Methods
TITLE OF INVENTION: Relating to Neurogenesis
FILE REFERENCE: 66778-356
CURRENT APPLICATION WUMBER: US/10/680,554
CURRENT FILING DATE: 2003-10-03
PRIOR FILING DATE: 2002-10-04 100.0%; Score 498; DB 15; 100.0%; Pred. No. 2.6e-45; tive 0; Mismatches 0; NUMBER OF SEQ ID NOS: 21 SOFTWARE: FastSEQ for Windows Version 4.0 SEQ ID NO 5 LENGTH: 86 86 61 CLPNLLCSRFPDGRYRCSMDLKNINF 86 61 CLPNLLCSRFPDGRYRCSMDLKNINF 86 61 CLPNLLCSRFPDGRYRCSMDLKNINF US-10-333-192-21 ; Sequence 21, Application US/10333192 ; Publication No. US20040077535A1 ; GENERAL INFORMATION: US-10-680-554-5
, Sequence S, Application US/10680554
; Publication No. US20040229291A1
; GENERAL INFORMATION: Query Match Best Local Similarity 100.0 Matches 86; Conservative , ORGANISM: Homo sapiens US-10-680-554-5 ; ORGANISM: Human US-10-333-192-21 TYPE: PRT TYPE: PRT ò



us-10-811-328-3.rpr

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Tue Nov
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GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

 protein search, using sw model OM protein

Run on:

November 7, 2005, 20:48:31; Search time 24.7186 Seconds (without alignments) 334.754 Million cell updates/sec

US-10-811-328-3 498 Title: Perfect score:

1 AVITGACERDVQCGAGTCCA.....CSRFPDGRYRCSMDLKNINF 86 Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:* Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description		rot		adhesive plaque pr	notch homolog - se	colipase precursor	tumor necrosis fac		MEGF6 protein - ra	hypothetical prote	colipase precursor	collagen, cuticula	granulin precursor	acrogranin - guine	hypothetical prote	notch 3 protein -	cysteine-rich prot	fibulin 1 precurso	fibulin 1 precurso	serine/threonine k	w	laminin gamma-1 ch	colipase precursor	nerve growth facto	mannosyl-oligosacc	65K early nonstruc	mannosyl-oligosacc	LR11 protein - mou	cadherin-related t
SUMMAKIES	I	1			2 A56175						2 T13576		2 S34665	1 GYHU							-	2 A42587	1 MMFFB2			2 A33901	1 WMBEDE	-	-	1 IJFFTM
	Length DB													593										112				1150		
	Query Match	20.2	17.8	16.3	15.6	15.1	14.7	14.6	14.4	14.4	14.4	14.3	14.3	14.3	14.2	14.2	14.2	14.1	13.9	13.9	13.8	13.8	13.8	13.7	13.7	13.7	13.7	13.7	13.7	13.7
	Score	100.5	88.5	81	77.5	75	73	72.5	71.5	71.5	71.5	71	71	71	70.5	70.5	70.5	70	69	69	68.5	68.5	68.5	68	68	9	68	69	68	68
	Result No.		~	٣	4	ß	ø	7	œ	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	29

protein F21H11.4 [probable membrane mouse developmenta hypothetical prote notch3 protein - h epithelin/granulin epithelin/granulin osteonidogen - hum alpha-2-macroglobu thrombospondin 2 p probable otsB prot laminin alpha-1 ch laminin alpha-1 ch laminin alpha-1 ch	hypothetical prote hypothetical prote
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C88450 S45463 1148653 1148653 S78549 C38128 B38128 B38128 C38128 S25111 T3HUP2 S25111 S107059 S18253	148324 T24293 T24294
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108 237 933 1620 2321 589 1376 4545 11327 11327 3075	722 802 949
6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6 6	13.22
666 665 665 665 665 665 665 665 665 665	655.5 65.55
0 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	4 4 4 5 4 5

ALIGNMENTS

RESULT 1

ALL PACLELL - LUMBERS (Man)
C;Species: Homo sapiens (man)
C;Species: Ordens: Jori188
R;Tsugi, T; Miyazaki, M.; Sakaguchi, M.; Inoue, Y.; Namba, M.
Biochem: Biophys. Res. Commun. 268, 20-24, 2000
A;Title: A REIC gene shows down-regulation in human immortalized cells and human tumor-A;Reference number: JC7188
A;Reference number: JC7188
A;Residues: JC7188
A;Residues: L-350 <TSU)
A;Residues: J-350 <TSU)
A;Residues: J-350 <TSU)
A;Residues: L-350 <TSU)
A;Residues: L-350 <TSU)
A;Residues: J-350 <TSU)
A;Residues: L-350 <TSU)
C;Comment: This protein is a secreted glycoprotein for head induction in amphibian embr
C;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: human REIC protein
C;Keywords: cardiac muscle; coiled coil; glycoprotein; heart; tumor REIC protein - human

4 Gaps 11; Query Match
Best Local Similarity 37.7%; Pred. No. 0.0038;
Matches 26; Conservative 3; Mismatches 29; Indels 11;

208 CDNQRDCQPGLCCAFQ---RGLLFPVCTPLPVEGELCHDPASRLLDLITWELEPDGALDR 264 7 CERDVOCGAGTCCAISLWLRGL--RMCTPLGREGEECH-PGSHKVPFFRKRKH-----HT 58 셤 ð

265 CPCASGLLC 273 59 CPCLPNLLC 67 g ð

RESULT 2

T08179

IRGS protein - Chlamydomonas reinhardtii

IRGS protein - Chlamydomonas reinhardtii

C;Species: Chan-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004

C;Accession: T08179

A;Reforence Chro. To. Beck.

A;Reforence number: Z16399

A;Reforence

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NyAlternate names: procollipase
C;Species: Homo saptens (man)
C;Date: 04-Dec-1986 #sequence_revision 19-May-1995 #text_change 09-Jul-2004
C;Species: Homo saptens (man)
C;Date: 04-Dec-1986 #sequence_revision 19-May-1995 #text_change 09-Jul-2004
C;Accession: A42568; A3349; A33163
R;Sims, H.F.; Lowe, M.E.
B;Ochemistry 31, 7120-7125, 1992
A;Title: The human colipase gene: isolation, thromosomal location, and tissue-specific e
A;Reference number: A42568 MUID:92353041; PMID:1643046
A;Accession: A42568
A;Molecule type: DNA
A;Residues: 1-112 <SIM>A;Accession: A2568
A;Molecule type: DNA
A;Residues: 1-112 <SIM>A;Residues: UCBIN:110576, NCBIN:110578, NCBIP:110580)|
R;Lowe, M.E.; Rosenblum, J.L.; McEwen, P.; Strauss, A.W.
B;Coss.reference extracted from NCBI backbone (NCBIN:110578, NCBIP:110580)|
R;Lowe, M.E.; Rosenblum, J.L.; McEwen, P.; Strauss, A.W.
B;Cohemistry 29, 823-828, 1990
A;Title: Cloning and characterization of the human colipase cDNA.
A;Reference number: A33949; MUID:90248429; PMID:2337598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C;Comment: Colipase, a cofactor of triacylglycerol lipase (EC 3.1.1.3), forms a 1:1 sto1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  notch homolog - sea urchin (Lytechinus variegatus)
C;Species: Lytechinus variegatus (variegated urchin)
C;Species: Lytechinus variegatus (variegated urchin)
C;Date: 22-Oct-1999 #sequence_revision 22-Oct-1999 #text_change 31-Jan-2000
C;Accession: T31070
R;Sherwood, D.R.; McClay, D.R.
A;Sherwood, D.R.; McClay, D.R.
A;Title: Identification and localization of a sea urchin Notch homologue: insights into A;Reference number: 220966; MUID:97454256; PMID:9310331
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AjCross-references: GB:J02883; NID:g180885; PIDN:AAA52054.1; PID:g180886
AjActe: evidence of partial N-g1ycosylation, possibly at Asn-43
R;Sternby, B.; Engstrom, A.; Hellman, U.; Vihert, A.M.; Sternby, N.H.; Borgstrom, Biochim. Biophys. Acta 784, 75-80, 1984
AjTtle: The primary sequence of human pancreatic colipase.
A;Reference number: A90652; MUID:84104937; PMID:6691986
A;Accession: A03163
                                                                                                                    A,Molecule type: mRNA
A,Residues: 1-2531 <SHE>
A,Cross-references: EMBL:AF000634; NID:g2570350; PID:g2570351; PIDN:AAB82088.1
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                                                     CERDVOCGAGTCCAISLWLRGLRMCTPLGREGEBCH-PGSHKVPFFRKRKHHTC---PCL 62
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Pred. No. 9.7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: preliminary; translated from GB/EMBL/DDBJ
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                                                                                                                                                                                                                                                                                                                                                         166 NKGRC--FPDGKTGYKC 180
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Best Local Similarity 29.9%;
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A; Residues: 1-112 < LOW>
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R;Rowen, L.; Mahairas, G.; Qin, S.; Ahearn, M.E.; Dankers, C.; Lasky, S.; Loretz, C.; Sc submitted to the EMBL Data Library, October 1997
A;Description: Sequence of the mouse major histocompatibility locus class III region.
A;Reference number: 216543
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Grossion: 170965
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Grossicon: 101964 «ROW»
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C;Grossicon: 11964 «ROW»
A;Grossicon: 11964 «ROW»
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A;Grossicon: 11964 «ROW»
C;Grossicon: 11964 «ROW»
A;Introns: 22/1; 49/2; 148/1; 264/1; 305/1; 384/1; 436/1; 501/1; 539/1; 577/1; 618/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1; 67/1;
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R. Innoue, K.; Takeuchi, Y.; Miki, D.; Odo, S.
J. Binoue, K.; Takeuchi, Y.; Miki, D.; Odo, S.
J. Binoue, K.; Takeuchi, Y.; Miki, D.; Odo, S.
J. Binoue, K.; Takeuchi, Y.; Miki, D.; Odo, S.
J. Binoue, K.; Takeuchi, Y.; Miki, D.; Odo, S.
A;Title: Mussel adhesive plaque protein gene is a novel member of epidermal growth factor and the constant 
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                                                                                                                                                                                                               13 CGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCPCLPNLLCSRF-- 70
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C;Species: Mus musculus (house mouse)
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     adhesive plaque protein Mgfp2 precursor - Mediterranean mussel
C;Species: Mytilus galloprovincialis (Mediterranean mussel)
C;Date: 27-Apr_1995 #sequence_revision 03-Oct-1995 #text_change 09-Jul-2004
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Score 88.5; DB 2; Length 640;
Pred. No. 0.11;
5; Mismatches 24; Indels 2:
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Query Match
Best Local Similarity 31.6%;
Matches 24; Conservative
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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on:

November 7, 2005, 20:47:46; Search time 117.413 Seconds (without alignments)

375.076 Million cell updates/sec

Title:

US-10-811-328-3

Perfect score: 498
Sequence:

1 AVITGACERDVQCGAGTCCA......CSRFPDGRYRCSMDLKNINF 86
Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
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Total number of hits satisfying chosen parameters: 1612378

1612378 seqs, 512079187 residues

Searched:

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : UniProt_03:*
 1: uniprot_sprot:*
 2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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% Query Match	100.0	99.6	86.7	62.3	61.0	57.4	57.0	55.9	54.3	53.7	53.3	53.3	51.1	50.9	50.9	50.1	50.1	49.5	22.5	21.8	21.6	21.6	20.9	20.5	20.3	20.3	20.3	•	20.3	20.2
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ALIGNMENTS

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R R R R R R R R R R R R R R R R R R R	Godowski P., Gfay A.; Godowski P., Gfay A.; "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: bioinformatics assessment."; Genome Res. 13:2265-2270(2003). [5]	rs
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similarity).
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                                                                                                                                                                                                    -!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Expressed in the steroidogenic glands, ovary,
testis, adrenal and placenta.
-!- SIMILARITY: Belongs to the prokinecitin family.
                                                                            Protein Sci. 13:2819-2824(2004).

-I- FUNCTION: Potently contract gastrointestinal (GI) smooth muscle. Induces proliferation, migration and fenestration (the formation of membrane discontinuities) in capillary endothelial cells derived from endocarine glands. Has little or no effect on a variety of other endothelial and non-endothelial cell types.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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PubMed=15340161; DOI=10.1110/ps.04682504;
Zhang Z., Henzel W.J.;
"Signal peptide prediction based on analysis of experimentally
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 105;
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Pfam; Pr06607; Prokineticin; 1.
Direct protein sequencing; Growth factor; Mitogen; Signal.
SIGNAL
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Last annotation update)
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By similarity.
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By similarity.
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EMBL; AY029225; AAK33111.1; -.
EMBL; AX358683; AAQ89046.1; -.
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01-MAR-2004 (TrEMBLrel. 26,
Prokineticin 1.
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Best Local Similarity 100..
Best Local Similarity 100..
                                                                verified cleavage sites.";
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Genew; HGNC:18454; PROK1.
H-InvDB; HIX0000868; -.
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105
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A Klausner R.D., Collins F.S., Wagner L., Ehenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haish F., Diatchenko L., Marusina K., Farrar A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.A., McEwan P.J., Mockertan K.J., Abramson R.D., Mullahy S.J., A Bosak S.A., McEwan P.J., McKertan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Andan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rzywinski M.I., Skalska U., Schmutz J., Myers R.N., Butterfield Y.S., Jones S.J., Marra M.A.;
Jones S.J., Marra M.A.;
T. "Generation and initial analysis of more than 15,000 full-length human and and moving CMM.
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SEQUENCE 2050031; PubMed=12054613; DOI=10.1016/S0006-291X(02)00239-5; MEDLINE=22050031; PubMed=12054613; DOI=10.1016/S0006-291X(02)00239-5; Medsuda Y., Takatsu Y., Tarao Y., Kumano S., Ishibashi Y., Suenaga M., Abe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S., Inatomi N., Ohtaki T., Onda H., Fujino M.;

Isolation and identification of EG-VEGF/prokineticins as cognate ilsochem. Biophys. Res. Commun. 293:396-402(2002).

Induces proliferation, migration and fenestration (the formation of membrane discontinuities) in capillary endothelial cells cof membrane discontinuities. In and inchesital cell types (By variety of other endothelial and non-endothelial cell types (By
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10-OCT-2003 (Rel. 42, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Prokineticin 1 precursor (Endocrine-gland-derived vascular endothelial growth factor) (EG-VEGF).
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
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Pred. No. 6.1e-45;
1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Strausberg R.; Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases. EMBL; BC025399; AAH25399.1; -. HSSP; P25687; IIMT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR009523; Prokineticin.
Pfam; PF06607; Prokineticin; 1.
SEQUENCE 105 AA; 11729 MW; E570FDE30EFB52D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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Matches 85; Conservative
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1 AVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKRK-HHTC 59
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81 AA;
         Query Match
Best Local Similarity
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                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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MEDLINE=22022134; PubMed=12024206; DOI=10.1038/417405a;
Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bermak J.C., Belluzzi J.,
Weaver D.R., Leelie F.M., Zhou Q.Y.;
"Prokineticin 2 transmits the behavioural circadian rhythm of the
suprachiasmatic nucleus.";
Nature 417:405-410(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
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Last annotation update)
           -!- SIMILARITY: Belongs to the prokinecitin family.
SUBCELLULAR LOCATION: Secreted (By similarity).
                                                                                                                                                                                                                                                                                                                                95.0%; Score 473; DB 1; 91.9%; Pred. No. 2.1e-42;
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GO; GO:0000187; P:activation of MAPK; IDA.
GO; GO:0001823; P:circadian rhythm; TAS.
GO; GO:0008284; P:positive regulation of cell;
GO; GO:0045765; P:regulation of anglogenesis;
InterPro; IPR009523; Prokineticin.
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By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
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                                                                                                                                                                                                                 Potential.
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Pfam; PF06607; Prokineticin; 1.
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NON TER 1 1 SEQUENCE 81 AA, 9192 MW; 7B1
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HSSP; P25687; 11MT.
                                                                                                                                    EMBL; AY089983; AAM09104.1; -.
HSSP; P25687; 11MT.
RGD; 620898; Prokl.
                                                                                                                                                                                                     Growth factor; Mitogen; Signal
                                                                                                                                                                                                                                                                                                         11642 MW;
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Matches 79; Conservative
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X MEDINE=98437381; PubMed=9761684; DOI=10.1006/jmbi.1998.2057;

A Boisbouvier J., Albrand J.-P., Blackledge M., Jaquinod M., Schweitz H., Lazdunski M., Marion D.; A structural Monologue of Colloguese in black mamba venom revealed by INMR floating disulphide bridge analysis.";

J. Mol. Biol. 283:205-219(1998).

J. Subcillular Location schreted.

--- Subcillular LOCATION: Screted.

--- SUBCILULARITY: Belongs to the prokinecitin family.

R DB; IIMT; NMR: @=1-81.

R Pfam; PF06607; Prokineticin.

R Pfam; PF06607; Prokineticin.

R Pfam; PF06607; Prokineticin.

R Pfam; PF06607; Prokineticin.

R Pfam; PF06607; Prokineticin.
                                                                                                                                                              CHARACTERIZATION.
MEDLINE=20036442; Pubmed=10567694; DOI=10.1016/S0014-5793(99)01459-3; Schweitz H., Pascaud P., Diochot S., Moinier D., Lazdunski M.; "MITI, a black mamba toxin with a new and highly potent activity on
                                                                                                                               6 ACERDVOCGAGTCCAISLWIRGIRMCTPLGREGEECHPGSHKVPFFRKRKHHTCPCLPNL
                                                                       Gaps
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"Snake venom. The amino acid sequence of protein A from Dendroaspis
polylepis polylepis (CK mamba) venom.";
Hoppe-Seyler's Z. Physiol. Chem. 361:1787-1794 (1980).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        30-MAY-2000 (Rel. 39, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Intestinal toxin 1 (MIT 1) (MIT1) (Venom protein A).
Dendroaspis polylepis polylepis (Black mamba).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea;
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            Length 81;
                                                                       Indels
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C -> S (in Ref. 1).
S -> C (in Ref. 1).
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86.7%; Score 432; DB 2; I
87.7%; Pred. No. 3.5e-38;
iive 5; Mismatches 5;
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MEDLINE=81115818; PubMed=7461607;
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Q863H5;
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1 AVITGACERDLQCGKGTCCAVSLWIKSVRVCTPVGTSGEDCHPASHKIPFSGQRKMHHTC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       28 AVITGACDRDPQCGGGMCCAVSLWVKSIRICTPMGKVGDSCHPWTRKVPFLGRRWHHTCP 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP
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MEDLINE=22050031; PubMed=12054613; DOI=10.1016/S0006-291X(02)00239-5;
MEDLINE=22050031; PubMed=12054613; DOI=10.1016/S0006-291X(02)00239-5;
Masuda Y., Takatsu Y., Terao Y., Kumano S., Ishibashi Y., Suenaga M.,
Abe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S.,
Inatomi N., Ohtaki T., Onda H., Fujino M.;
Isolation and identification of Eq-VEGF/prokineticins as cognate
ligands for two orphan G-protein-coupled receptors.";
Biochem. Biophys. Res. Commun. 293:396-402(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus.
                                                                                                                                                                                                                                                                                                                                                         Bos taurus (Bovine).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUB=Testis;

BELLINE-25612805; PubMed=12728244; DOI=10.1038/sj.embor.embor830;
Kaser A., Winklmayr M., Lepperdinger G., Kreil G.;

"The AVIT protein family.";

"The AVIT protein family.";

EMBO Rep. 4:469-473(2003).

EMBL; AX195558; AAP31907.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61.0%; Score 304; DB 2; Length 108; 62.3%; Pred. No. 1.6e-24; ive 11; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EFFECT ON CIRCADIAN LOCOMOTOR ACTIVITY.
MEDLINE=22022134; PubMed=12024206; DOI=10.1038/417405a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam; PF06607; Prokineticin; 1.
SEQUENCE 108 AA; 11672 MW; C00410399A9B215E CRC64;
                                                                                                                                                                                                                                                                                    01-JUN-2003 (TrEMBLrel. 24, Last sequence update) 01-MAR-2004 (TrEMBLrel. 26, Last annotation update) Bv8/prokineticin 2-like protein splice variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 28-FEE-2003 (Rel. 41, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                         108 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nterPro; IPR009523; Prokineticin.
                                                                                                           78
                                                                  77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Prokineticin 2 precursor (PK2).
Name=Prok2; Synonyms=Bv8;
Rattus norvegicus (Rat).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88 CLPGLACSRISFNRYIC 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CLPNLLCSRFPDGRYRC 77
                                                                                             | | | | | | : ::| PCAPNLACVQTSPKKFKC
                                                                  60 PCLPNLLCSRFPDGRYRC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity 62.3%
                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Bovinae; Bos
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Q863H4
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation. the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 09
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                                                                                                                                                  -!- FUNCTION: May function as an output molecule from the suprachiasmatic nucleus (SCN) that transmits behavioral circadian rhythm. May also function locally within the SCN to synchronize output. Potently contracts gastrointestinal (GI) smooth muscle (B)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP
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                                                                                                                                                                                                                                                                                               -!- SUBCELLULAR LOCATION: Secreted (By similarity).
-!- TISSUE SPECIFICITY: Expressed at high levels in testis and at lower levels in brain, lung, ovary, spleen, thymus and uterus.
-!- INDUCTION: Activated by CLOCK and BML1 heterodimers and light; inhibited by period genes (FRI, PER2 and PER3) and cryptochrome genes (CRY1 and CRY2) (Probable).
-!- SIMILARITY: Belongs to the prokinecitin family.
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         C., Lee A.G., Bermak J.C., Belluzzi J.,
u Q.-Y.;
Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bermak J.C., Belluzzi J Weaver D.R., Leslie F.M., Zhou Q.-Y.; Prokineticin 2 transmits the behavioural circadian rhythm of the suprachlaematic nucleus."; Nature 417:405-410 (2002).
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IISSUB=Testis;
TISSUB=Testis;
Fig. 10.1038/sj.embor.embor830;
Kaser A., Winklmayr M., Lepperdinger G., Kreil G.;
"The AVIT protein family.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Eutheria, Cetartiodactyla, Ruminantia, Pecora, Bovidae,
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
Bv8/prokineticin 2-like protein.
Bos taurus (Bovine).
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57.1%; Pred. No. 1.2e-22;
ive 15; Mismatches 18
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By similarity.
By similarity.
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By similarity.
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Prokineticin 2.
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Pfam; PF06607; Prokineticin; 1.
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107
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MBDLINE=22515712; PubMed=12628381; DOI=10.1016/S1096-4959(02)00294-4;
Lai R., Liu H., Lee W.H., Zhang Y.;
"Two novel Bv8-like peptides from skin secretions of the toad Bombina
                                            GO; GO:0001664; F:G-protein-coupled receptor binding; ISS.
GO; GO:0001664; F:G-protein-coupled receptor binding; ISS.
GO; GO:0001525; P:activation of MAPK; ISS.
R GO; GO:0001525; P:anti-apoptosis; ISS.
R GO; GO:0006918; P:cell proliferation; ISS.
R GO; GO:0007204; P:cytosolic calcium ion concentration elevation; ISS.
R GO; GO:0007204; P:cytosolic calcium ion concentration elevation; ISS.
R GO; GO:0007323; P:perception coupled receptor protein signalin. .; ISR GO; GO:0004923; P:perception of pain; ISS.
R GO; GO:0004923; P:perception of pain; ISS.
R GO; GO:0004933; P:perception of pain; ISS.
R GO; GO:0004933; P:perception of pain; ISS.
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
By8 protein homolog 2.
By8 protein homolog 2.
Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Archeobatrachia; Bombina.
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 134:509-514(2003).
EMBL; AF411091; AAN03822.1; -.
HNSP; P25687; 11MT.
InterPro; IPR009523; Prokineticin.
Pfam; PF06607; Prokineticin; 1.
SEQUENCE 96 AA; 10198 MW; EC4BAA5EFE49B2F0 CRC64;
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49.5%; Pred. No. 2.4e-22;
ive 11; Mismatches 18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                              1 AVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSH--
                                                                                                                                                                                                                                                                                                      PF06607; Prokineticin; 1.
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Rep. 4:469-473(2003).
AY192557; AAP31906.1;
P25687; 11MT.
                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 49.5%
es 48; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@ib-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Isold=Q9HC23-2; Sequence=VSP 005219;
TISSUE SPECIFICITY: Expressed in the testis and, at low levels, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        verified cleavage sites.";

Protein Sci. 13:2819-2824 (2004).

-!- FUNCTION: May function as an output molecule from the suprachiasmatic nucleus (SCN) that transmits behavioral circadian rhythm. May also function locally within the SCN to synchronize output. Potently contracts gastrointestinal (GI) smooth muscle.
-!- SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GC:0000187; P:activation of MAPK; TAS.
GO:0001525; P:angiogenesis; IDA.
GO:0006916; P:anti-apoptosis; IDA.
GO:00068283; P:cell prolitation; IDA.
GO:0006935; P:chemotaxis; IDA.
GO:0007204; P:cytosolic calcium ion concentration elevation; TAS.
                                                                                                                                                                                                                                                    MEDLINE=20047850; PubMed=10580115; DOI=10.1016/S0014-5793(99)01473-8; Wechelberger C., Puglisi R., Lepperdinger G., Boitani C., Kreil G.; "The mammalian homologue of Bv8 from frog skin is mainly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                INDUCTION. Activated by CLOCK and BMAL1 heterodimers and light; inhibited by period genes (PER1, PER2 and PER3) and cryptochrome genes (CRY1 and CRY2) (Probable).
SIMILARITY: Belongs to the prokinecitin family.
                                                                                                                            Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                    [2]
SEQUENCE FROM N.A. (ISOFORM 2).
MEDLINE=21160229; PubMed=11259612;
Li M., Bullock C.M., Knauer D.J., Ehlert F.J., Zhou Q.-Y.;
Lidentification of two prokineticin cDNAs: recombinant proteins potently contract gastrointestinal smooth muscle.";
Mol. Pharmacol. 59:692-698(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         snang z., Henzel W.J.; signal peptide prediction based on analysis of experimentally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          receptor binding;
                                                     16-OCT-2001 (Rel. 40, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Protineticin 2 precursor (PK2) (Protein Bv8 homolog).
Name=PROX2; Synonyms=BV8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Event=Alternative splicing; Named isoforms=2;
129 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GO:0005576; C:extracellular; TAS.
GO:0001664; F:G-protein-coupled recept
GO:000187; P:activation of MAPK; TAS.
GO:0001525; P:angiogenesis; IDA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 28-42.
PubMed=15340161; DOI=10.1110/ps.04682504; Zhang Z., Henzel W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=1;
IsoId=Q9HC23-1; Sequence=Displayed;
                                                                                                                                                                                                                      SEQUENCE OF 5-129 FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF182069; AAG16893.2; -.
EMBL; AF333025; AAK49919.1; -.
                                      (Rel. 40, Created)
                                                                                                                                                                                                                                                                                                                                 FEBS Lett. 462:177-181(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the small intestine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HGNC:18455; PROK2
   STANDARD;
                                                                                                                                                                                 NCBI_TaxID=9606;
                                                                                                                                                                                                                                           TISSUE=Testis;
                                                                                                                                                                                                                                                                                                                   spermatocytes.
                                      16-OCT-2001
   HUMAN
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Genew;
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RESULT 10

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                                                                                                                                       Query Match
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GO; GO:0007186; P:G-protein coupled receptor protein signalin. . .; NAS. GO; GO:0006594; P:inflammatory response; NAS. GO; GO:0019233; P:perception of pain; TAS. GO; GO:0019239; P:perception of pain; TAS. GO; GO:0045987; P:positive requiation of smooth muscle contra. . .; IDA. GO; GO:0007283; P:spermatogenesis; IMP. InterPro; IPR00552; Prokineticin. Pfam; PF06607; Prokineticin. 1. Alternative splicing; Biological rhythms; Direct protein sequencing; Neuropeptide; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                       28 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPWGKLGDSCHPLTRKNNFGNGRQERRKR 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE-Skin secretion:
MEDLINE-9934621; PubMed=10422759; DOI=10.1016/S0014-2999(99)00229-0;
MADLINE-99349621; PubMed=10422759; DOI=10.1016/S0014-2999(99)00229-0;
MADLIAY C., Wechselberger C., Mignogna G., Negri L., Melhiorri P.,
Barra D., Kreil G.;
                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein Bv8 precursor.
Bombina variegata (Yellow-bellied toad).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi;
Amphibia, Batrachia; Anura; Archeobatrachia, Bombinatoridae; Bombina.
NCBI_TaxID=8348;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     venom induce hyperalgesia in rats.";
Eur. J. Pharmacol. 374:189-196(1999).
-!- FUNCTION: Potently contract gastrointestinal (GI) smooth muscle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Bv8, a small protein from frog skin and its homologue from snake
                                                                                                                                                                                                                                                                                                                                                                                   21;
                                                                                                                                                                                                                                                                                                                                                   54.3%; Score 270.5; DB 1; Length 129; 45.9%; Pred. No. 6.5e-21;
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                                                                                                                                                                       Prokineticin 2.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
Kinilarity.
Kinilarity.
Wissing (in isoform 2).
KridevSP 005219.
W; 0487679E8700DA55 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                     1 AVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Induces hyperalgesia.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SIMILARITY: Belongs to the prokinecitin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         88 KRSKRKKEVPFFGRRMHHTCPCLPGLACLRTSFNRFIC 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       48 ------VPFFRKRKHHTCPCLPNLLCSRFPDGRYRC 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                     45; Conservative 14; Mismatches
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Pfam, PF06607, Prokineticin, 1.
Direct protein sequencing, Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AF168790; AAD45816.1; -.
                                                                                                                                                                                                                                                                                                                 129 AA; 14314 MW;
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107
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Best Local Similarity
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STRAIN=CS7BL/60; TISSUB=Testis; MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266; MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266; MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266; Mikaido R., Saitor R., Suzuki H., Yamanaka I., Kiyosawa H., Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schriml L.M., Kanapin A., Matsuda H., Chothia C., Corbani L.E., Cousins S., Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., Gasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L., Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    20 AVITGACDKDVQCGSGTCCAASAWSRNIRFCIPLGNSGEDCHPASHKVPYDGKRLSSLCP
                                                                                                                                                                                                                                                                                                                                                                                                                        1 AVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-2004/850; PubMed=10580115; DOI=10.1016/S0014-5793(99)01473-8; Wechselberger C., Puglisi R., Lepperdinger G., Boitani C., Kreil G.; "The mammallan homologue of Bv8 from frog skin is mainly expressed in
                                                                                                                                                                                                                                                                                                                                                             Gaps
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MEDLINE=22022134; PubMed=12024206; DOI=10.1038/417405a;
Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bermak J.C., Belluzzi J.,
Weaver D.R., Leslie F.M., Zhou Q.-Y.;
"Prokineticin 2 transmits the behavioural circadian rhythm of the
suprachiasmatic nucleus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jilek A., Engel E., Beier D., Lepperdinger G.; "Murine Bv8 gene maps near a synteny breakpoint of mouse chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                             1;
                                                                                                                                                                                                                                                                                Score 267.5; DB 1; Length 96; Pred. No. 1e-20;
                                                                                                                                                                                                                                                                                                                                                      21; Indels
                                                                                                                                                                             y similarity.
A12490A7437609B4 CRC64;
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09QXU7; 09QXU5; Q9QXU6;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 44, Last sequence update)
05-UUL-2004 (Rel. 44, Last annotation update)
Prokineticin 2 precursor (PK2) (Protein Bv8 homolog).
Name=Prok?; Synonyms=Bv8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN=129/SvJ;
Pubmed=11054548; DOI=10.1016/S0378-1119(00)00355-3;
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                             By similarity.
By similarity.
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       Protein Bv8.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 CLPNLLCSRFPDGRYRCS 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 CKSGLTCSKSGE-KFKCS 96
96
38
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78
86
95
10102 MW;
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                                                                                                                                                                                                                                                                                53.7%;
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                                                                                                                                                                                                              96 AA;
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7, 2005, 20:44:40; Search time 114.467 Seconds (without alignments) 273.682 Million cell updates/sec
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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Maximum DB seq length: 200000000
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461
                                                                                                                  November
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                                                                                                                                                                                             Title:
Perfect score:
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                                                                           OM protein
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

geneseqp2001s:*
geneseqp2002s:*
geneseqp2003as:* A Geneseq 16Dec04:* 1: qeneseqp1980s:* geneseqp1980s:* geneseqp1990s:* geneseqp2000s:* geneseqp2004s: Database

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	de			SUMMARIES		
	Query Match	Query Match Length DB	DB	ID	Description	c
	100.0	81	5	ABG94398	Abg94398 Hu	Human GPC
	100.0	81	Ŋ	AA015530		Human phy
	100.0	81	Ŋ	AAE24385	Aae24385 Hu	Human pro
	100.0	81	7	ADD69041	Add69041 Hu	Human Bv8
	100.0	81	7	AD005356	Ado05356 Hu	Human maj
	100.0	81	œ	ADN43258	•	Amino aci
	100.0	81	œ	ADR24005	Adr24005 Hu	Human ZAQ
	100.0	108	4	AAB68426	Aab68426 Am	Amino aci
	100.0	108	z,	ABG94397	_	Human GPC
461	100.0	108	2	AA015531	Aao15531 Hu	Human phy
461	100.0	108	ß	AAE24384	Aae24384 Hu	Human pro
461	100.0	108	9	ABU07602		Human ZVE
461	100.0	108	9	AAE36789		Human Bv8
461	100.0		7	ADD69039		Human Bv8
461	100.0	108	7	ADF28067	_	Human Zve
461	100.0	108	7	ABG75087	Abg75087 Hu	Human pro
_	100.0	108	7	ADJ71811		Human pro
461	100.0		ω	ADN41839	-	Amino aci
461	100.0	108	œ	AD024421	Ado24421 Ht	Human PRO
461	100.0	108	α	ADS86957	Ads86957 Ht	Human 2ve
	100.0	108	œ	ADS00460	Ads00460 Ht	Human Bv8
461	100.0	116	œ	ADN41861	Adn41861 An	Amino aci
461	100.0	116	œ	ADS86981	_	Human Zve
456	98.9		Ŋ	ABG94400	_	C-termina
456	98.9	80	7	ADD69044	Add69044 Ht	Human Bv8

Rat G		Abg94401 Rat GPCR Abb6962 Rat G pro Aae36790 Mouse Bv8 Adf8059 Bat Bv8	Murine Murine Amino	Adj71808 Human Bv8 Aas3788 Human Bv8 Adj71815 Human Dr0 Adn41864 Amino aci Ads86984 Human Zve Ads00458 Human Bv8
ABG94402 ABB06963 ADD69061	ADO05358 ADN43260 ADN43262 ABG94408	ABG94401 ABB06962 AAE36790	ADD69059 ADD69077 ADS00462 ADN43257	ADJ71808 AAE36788 ADJ71815 ADN41864 ADS86984 ADS00458
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81 81 81	81 81 81	107	107 107 102	124 129 129 129 129
96.5 96.5 96.5	96.99 96.59 86.55	996.99 86.59	96.5 96.5 6.5 6.5	95.6 95.6 95.6 95.6
445 445 445	4 4 4 4 4 4 4 4 7 7 7 7 7	2444 2445 3	445 445 445 440.5	4440.5 4440.5 440.5 740.5 70.5 70.5
26 27 28	8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8	9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9 9	9 9 9 9 9 9 9 9 9 9	4 4 4 4 4 4 0 4 5 6 4 5

ALIGNMENTS

G-protein coupled receptor; GPCR; ZAQ; human; ZAQC; ZAQT; rat; ZAQ1; rZAQ1; rZAQ2; mouse; I5E receptor; mI5E; GPR73; Bv8 protein; MIT1; digestive disorder; central nervous system disorder; CRS; diarrhoea; bowel inflammation; constipation; food absorption disorder; nootropic; Alzheimer's disease; Parkinson's disease; schizophrenia; laxative; antiinflammatory; antidiarrhoeic; neuroleptic; neuroprotective; receptor. Human GPCR ligand Bv8 protein sequence #2. Ź ABG94398 standard; protein; 81 (first entry) 27-NOV-2002 ABG94398; RESULT 1 ABG94398

WO200262944-A2.

Homo sapiens

15-AUG-2002.

01-FEB-2002; 2002WO-JP000852.

02-FEB-2001; 2001JP-00026820.

(TAKE) TAKEDA CHEM IND LTD

Watanabe T, Terao Y, Shintani Y; Takatsu Y, Masuda Y, Ohtaki T, Hinuma S;

WPI; 2002-627537/67. N-PSDB; ABS71104.

Screening of compounds modifying the binding of G-protein coupled receptor protein ZAQ and related proteins to their ligands for use in treatment and diagnosis of digestive disorders.

Claim 1; Page 165; 197pp; Japanese.

The present invention relates to a screening method for compounds for their ability to modify the binding of G-protein coupled receptor (GPCR) protein ZAQ and related proteins (human ZAQC, human ZAQT, rat ZAQ1 (rZAQ1), rZAQ2, human and mouse ISE (mISB) receptor, and mouse GPR33) to their ligands (the mature form of human, mouse or rat Bv8 protein). The receptor protein and ligand are contacted in the presence or absence of the test compound. The compounds are useful in a drug composition for the

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention comprises a method for producing an active peptide that has the same activity as a ZAQ ligand isolated from eukaryotic cells. The method of the invention is useful for the production of a physiologically active ZAQ ligand for use in preventing or treating digestive diseases (e.g. colitis and diarrhea). The present amino acid sequence represents a human physiologically active ZAQ ligand-related protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Industrial production of physiologically-active ZAQ ligand by expressing in transformant prokaryote and refolding in redox buffer, for use in preventing or treating digestive diseases e.g. colitis and diarrhea.
treatment, and prevention of digestive and central nervous system (CNS) disorders, including bowel inflammation, diarrhose, constipation, food absorption disorders, Alzheimer's disease, Parkinson's disease and schizophrenia. The present sequence represents a GPCR or related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; ZAQ ligand; physiologically-active ZAQ ligand; digestive disease; colitis; diarrhoea.
                                                                                                                                                                                                 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPWGKLGDSCHPLTRKVPFFGRRMHHTCP
                                                                                                                                                                                 1 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP
                                                                                                                                                 Gaps
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                                                                                                                Length 81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human physiologically-active ZAQ ligand-related protein 5.
                                                                                                                                             Indels
                                                                                                                / Match 100.0%; Score 461; DB 5; Local Similarity 100.0%; Pred. No. 3.2e-41; nes 81; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; Score 461; DB 5;
; Pred. No. 3.2e-41;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                    CLPGLACLRTSFNRFICLAQK
                                                                                                                                                                                                                                                                                                                                                                 AAO15530 standard; protein; 81
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1 Similarity 100.0%;
81; Conservative 0;
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                                                                                  Sequence 81 AA;
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                                                                                                                Query Match
Best Local Si
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The invention relates to human prokineticin 1 and 2 polypeptides that stimulate gastrointestinal smooth muscle contraction and nucleic acid molecules encoding such polypeptides. Polypeptides of the invention are useful for treating disorders involving impaired gastrointestinal motility. They are useful for stimulating gastrointestinal motility in operational ileus, chronic constipation and gastrointestinal reflux disease. The prokineticin antagonists are useful for inhibiting gastrointestinal necility in conditions bf diarrhoea, malabsorptive disorders, inflammatory bowel disorders, inflectious diseases and intestinal cancers. The antagonists also act as analgesics. The present sequence is human prokineticin 2 mature protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New isolated human prokineticin 1 and 2 polypeptides that stimulate gastrointestinal smooth muscle contraction, useful for improving impaired gastrointestinal motility in irritable bowel syndrome, chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AVITGACDKDSQCGGGGCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP
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                                                                                                                                                                                                                                         Human, prokineticin 2, gastrointestinal motility, intestinal cancer; irritable bowel syndrome; gastrointestinal reflux disease, diarrhoea; diabetic gastroparesis; chronic constipation; malabsorptive disorder; inflammatory bowel disorder; analgesic; infectious disease.
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100.0%; Pred. No. 3.2e-41;
ive 0; Mismatches 0;
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CLPGLACLRTSFNRFICLAOK
                CLPGLACLRISFNRFICLAQK
                                                                                                            AAE24385 standard; protein; 81
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N-PSDB; AAD39322.
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CLPGLACLRTSFNRFICLAQK

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1 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP

RESULT

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major human PK2
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                                                                  WO2003088904-A2
                                                 Homo sapiens
                                                                                     30-OCT-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human; prokineticin 2; PK2; circadian rhythm; modulation; drug screening; circadian rhythm disorder; non-24-hour sleep-wake syndrome; rapid time-zone change syndrome; jetlag; work-shift syndrome; delayed phase sleep syndrome; advanced sleep phase syndrome;
                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel angiogenesis inhibitor comprising a compound that inhibits the activity of an amino acid sequence given in the specification. Angiogenesis-related proteins Bv8, ZAQ and ISE were utilised within the method of the invention. The molecules of the invention demonstrate cytostatic and antiinflammatory activities whilst the method may be useful for treatment and prevention of cancer, ovarian diseases, diabetic retinopathy and inflammatory disease. The current sequence is that of the human Bv8-related protein of the invention.
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                                                                                                                                                                                                                                                                                                    Angiogenesis inhibitors for treatment and prevention of cancer, ovarian
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                                                                                       angiogenesis inhibitor; cytostatic; antiinflammatory; cancer; ovarian disease; diabetic retinopathy; inflammatory; ZAQ; Bv8; I5E;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 81;
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100.0%; Pred. No. 3.2e-41;
trive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human major prokineticin 2 (PK2), SEQ ID NO:5.
                                                                                                                                                                                                                                                                                                                                  Claim 1; SEQ ID NO 19; 308pp; Japanese.
                                                                    Human Bv8-related protein - SEQ ID 19
                                                                                                                                                                                                                                                                                                               diseases and inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADO05356 standard; protein; 81 AA
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            ADD69041 standard; protein; 81 AA
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                                                                                                                                                                                          03-FEB-2003; 2003WO-JP001057
                                                                                                                                                                                                              04-FEB-2002; 2002JP-00027299
                                                                                                                                                                                                                                  (TAKE ) TAKEDA CHEM IND LTD.
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                                                   (first entry)
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                                                                                                                                                                                                                                                      Ohtaki T, Masuda Y,
                                                                                                                                                                                                                                                                        WPI; 2003-646310/61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                   N-PSDB; ADD69042.
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                                                                                                                                                   WO2003066860-A1
                                                                                                                                 Homo sapiens.
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Matches 81;
                                                  15-JAN-2004
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                                ADD69041;
                                                                                                              human.
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The invention relates to a method of screening for a compound for its ability to modulate circadian rhythm. The method involved determining the cability of a prokination 2 (PKZ) receptor agonist or antagonist to modulate one or more indicia or circadian rhythm function. The compound is identified as being a PKZ receptor agonist or antagonist to modulate one or more indicia or circadian rhythm function. The compound complisation produced by the interaction of PKZ and a receptor selected from the PKZ receptor (e.g., ADDO5353) or the invention is based on the findings that PKZ expression in the suprachiasmatic nucleus (SCM) oscillates in a circadian rhythm of the suprachiasmatic nucleus (SCM) oscillates in a circadian rhythm of an animal by administration of a PKZ receptor antagonist or agonist; a composition comprising detectably labelled PKZ and an isolated mouse composition comprising a detectably labelled PKZ and an isolated mouse composition comprising detectably labelled PKZ and an isolated mouse composition comprising detectably labelled PKZ and an isolated mouse composition comprising a detectably labelled PKZ and an isolated mouse composition comprising a detectably labelled PKZ and an isolated mouse composition and and for somethous of such constructs vectors and host cells comprising circadian rhythm and for the light regulated expression of a nucleic according in the invention are useful for identifying compounds for methods of the invention are useful for identifying compounds for methods of the invention are useful for identifying compounds compounds of the invention are useful for identifying compounds for methods of circadian rhythm disorders such as an off-24-hour sleep-wake sprudrome, devanced sleep, and PKZ receptor agonists which promote sleep, and PKZ receptor agonists which promote sleep, phase sleep phase sleep syndrome, advanced sleep phase syndrome associated with decreased amplit
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irregular sleep-wake pattern syndrome; decreased amplitude syndrome; seasonal affective disorder; ultradian rhythm; daydreaming; urination; hunger; infardian rhythm; female sexual receptivity; CNS; central nervous syndrome; PK2 receptor antagonist; PK2 receptor agonist.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Screening for compounds for modulating circadian rhythm, for treating seasonal disorders, comprises determining ability of prokineticin-2 receptor antagonist or agonist to modulate one or more circadian rhythm function indicia.
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the invention relates to a monoclonal antibody (I) having high avidity to human ZAQL-1 ligand polypeptides, comprising either of two fully defined sequences of 86 amino acids (S1). (I) is ZLI-107a or ZLI-234 a produced sequences of 86 amino acids (S1). (I) is ZLI-107a or ZLI-234 a produced comparing out assay of the polypeptide containing (S1) which involves reacting (I) with the test-liquid containing (B1) which involves reacting (I) with the test-liquid containing (B1) which is salt, and measuring the ratio of the polypeptide bound to (I). (I) is useful as a diagnostic or therapeutic agent for diagnosis and/or treatment of diseases such as endometrial cancer, endometriosis or covulation disorders, digestive diseases, diseases associated with angiogenesis, diseases relating to pregnancy, eating disorder, sleeping disorder, seasonal depression, reproductive dysfunction, endocrine of seasons and contained the contained the cerebral circulatory disorder, sieases, various disorders caused by aging, anxiety, depression, manic depression, schizophrenia,
                                                                                                                                                                            anticonvulent; antidepreseant; antidiabetic; anti-HIV; antimanic; antiparkingoniant; antidepreseant; antidiabetic; anti-HIV; antimanic; antiparkingonian; cerebroprotective; cytostatic; eating disorders; endocrine; gastrointestinal; gynecological; hypotensive; neuroprotective; nootropic; ophthalmological; tranquilizer; vasotropic; vulnerary; monoclonal antibody; human; ZAQL-1; ligand; hybridoma cell; assay; diagnosis; endometrial cancer; endometriosis; ovulation disorder; diagnosis; endometrial depression; reproductive dysfunction; endocrine disease; senile dementia; reproductive dysfunction; endocrine disease; senile dementia; spinal injury; epilepsy; anxiety; depression; schizophrenia; alcoholism; parkinson's disease; hypertension; arteriosclerosis; arrhythmia; premenstrual disorder syndrome; glaucoma; AIDS; diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alcoholism, Parkinson's disease, hypertension, arteriosclerosis, arrhythmia, premenstrual disorder syndrome, glaucoma, AIDS, diabetes, etc. This sequence corresponds to a ZAQ-1 ligand associated protein used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               monoclonal antibody having high avidity to human ZAQL-1 polypeptide,
                                                                                                                                                         antiangiogenic, antialcoholic, antiarrhythmic, antiarteriosclerotic,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          useful for preventing, treating or diagnosing diseases such as
endometrial cancer, ovulation disorders, Alzheimer's disease, AIDS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 461; DB 8;
100.0%; Pred. No. 3.2e-41;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Horikoshi Y, Masuda Y,
                                                                                                       Human ZAQ-1 ligand-associated protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; SEQ ID NO 3; 64pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Parkinson's disease and diabetes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21-JAN-2004; 2004WO-JP000498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-JAN-2003; 2003JP-00014055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (TAKE ) TAKEDA CHEM IND LTD.
                                                   21-OCT-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        81; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2004-593431/57.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO2004065419-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 81 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matsumoto H,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-AUG-2004.
ADR24005;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Loca
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The specification describes a method for identifying a compound that modulates neurogenesis. The method comprises providing a compound that modulates prokineticin receptor (PRR) signaling, contacting a neural stem corporation or progenitor cell with the compound, and determining the ability of the neurogenesis or for identifying compounds that modulate neurogenesis. The method is useful for modulating neurogenesis or for identifying compounds that modulate neurogenesis. These are used for both ex vivo or in vivo therapeutic applications where neural regeneration is desirable, such as in Alzheimer's disease, parkinen's disease. The parkinen's disease or other debilitating neurodespenerative diseases. The present sequence represents human prokineticin 2 (PRZ) isoform 2, which may be used in the method of the invention to modulate neurogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Identifying a compound that modulates neurogenesis comprises contacting a neural stem or progenitor cell with a compound that modulates prokineticin receptor signaling and determining its ability to modulate neurogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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                                                                                                                                                                                                                                                                                                                                                                                         neurogenesis, prokineticin receptor; PKR; neural stem; progenitor cell; neural regeneration; Alzheimer's disease; Parkinson's disease; neurodegenerative disease; prokineticin 2; PK2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AVITGACDKDSQCGGGGCAVSIWIKITIHIHIHIHIHIHIHIHIHITCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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0
                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of human prokineticin 2 (PK2) isoform 2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 81;
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100.0%; Pred. No. 3.2e-41;
iive 0; Mismatches 0;
81
                           61 CLPGLACLRTSFNRFICLAOK 81
                                                                                                                                                                                 ADN43258 standard; protein; 81 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 26; Fig 6B; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLPGLACLRTSFNRFICLAOK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-OCT-2003; 2003WO-US031626,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-OCT-2002; 2002US-0416202P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
Local 81; Conservative
The B1; Conservative
                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2004-340794/31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cheng MY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2004032851-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 81 AA;
                                                                                                                                                                                                                                                                                         15-JUL-2004
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Zhou Q,

Ohtaki T;

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Gaps

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Length 81; Indels 9 9

AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP 1 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP

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ADR24005 ID ADR24005 standard; protein; 81 AA.

RESULT 7

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The present sequence represents a human Zven1 polypeptide. The Zven1 gene is present on chromosome 3p21.1-3p14.3. The specification also describes is present on chromosome 3p21.1-3p14.3. The specification also describes Zven2. Zven polymocleotides and polypeptides are useful in veterinary and human therapeutics, for treating small cell cancer of the lung, to bromote wound healing, to prevent or to treat an adverse reaction of the promote wound healing, to prevent or a skin-irritating agent, to stimulate the immune system of an immunocompromised individual, as antitumour agents, as antiinflammatory agents, as agents to regulate regeneration or remodeling of tissue, as agents to modulate necrosis or tissue growth developmental arrest, to inhibit proliferation of tumour cells, cellular differentiation and necrosis, to treat disorders associated with agestrointestinal cell contractility, secretion of digestive enzymes and caids agents and crohn's disease
                                                                                                                                                                                                                                                               Zvenl; 3p21.1; 3p14.3; Zven2; small cell lung cancer; wound healing;
antitumour; antiinflammatory; necrosis; tissue growth; digestive enzyme;
cellular differentiation; gastrointestinal cell contractility;
gastrointestinal motility; inflammation; hypermotility; diarrhoea;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel isolated Zven polypeptide useful for inhibiting proliferation of tumor cells, for treating small cell cancer of lung, to promote wound healing, and for treating Crohn's disease and diarrhea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Thompson PP;
                                                                                                                                                                                                                                 Amino acid sequence of a human Zvenl polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sheppard PO, Bishop PD, Whitmore TE,
                                                                                                                         Z
                    61 CLPGLACLRTSFNRFICLAQK 81
81
                                                                                                                           AAB68426 standard; protein; 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 3; 98pp; English
CLPGLACLRISFNRFICLAOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-NOV-1999; 99US-00442164.
25-FEB-2000; 2000US-00511879.
19-APR-2000; 2000US-00552203.
07-UUN-2000; 2000US-0210332P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            14-NOV-2000; 2000WO-US031278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (ZYMO ) ZYMOGENETICS INC.,
                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB; AAF85368
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                                                                                                                                                                                                                                                                                                                                                Crohn's disease
                                                                                                                                                                                                                                                                                                                                                                                                                      WO200136465-A2
                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                 23-JUL-2001
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   61
                                                                                                                                                             AAB68426;
                                                                                                      AAB68420
                                                                                       RESULT
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The present invention relates to a screening method for compounds for their ability to modify the binding of G-protein coupled receptor (GPCR) protein ZAQ and related proteins (human ZACC, human ZAQT, rat ZAQI (TZAQI), rZAQ2, human and mouse ISE (mIE) receptor, and mouse GPR73) to receptor protein and ligand are contacted in the presence or absence of the test compound. The compounds are useful in a drug composition for the treatment, and prevention of digestive and central nervous system (CNS) disorders, including bowel inflammation, diarrhoea, constipation, food absorption disorders, Alabeimer's disease, Parkinson's disease and
                                                                                                                                                                                                                                          G-protein coupled receptor; GPCR; ZAQ; human; ZAQC; ZAQT; rat; ZAQ1; rZAQ1; rZAQ2; mouse; ISE receptor; mISE; GPR73; Bv8 protein; MIT1; digestive disorder; central nervous system disorder; CMS; diarrhoea; bowel inflammation; constipation; food absorption disorder; nootropic; Alzheimer's disease; Parkinson's disease; schizophrenia; laxative; antiinflammatory; antidiarrhoeic; neuroleptic; neuroprotective; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    schizophrenia. The present sequence represents a GPCR or related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AVITGACDKDSQCGGGGCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Screening of compounds modifying the binding of G-protein coupled receptor protein ZAQ and related proteins to their ligands for use in treatment and diagnosis of digestive disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Watanabe T, Terao Y, Shintani Y;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 461; DB 5;
100.0%; Pred. No. 4.3e-41;
iive 0; Mismatches 0;
                                                                                                                                                                                                               Human GPCR ligand Bv8 protein sequence #1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 3; Page 164; 197pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLPGLACLRTSFNRFICLAQK 108
                     CLPGLACLRTSFNRFICLAQK 108
                                                                                                              ABG94397 standard; protein; 108 AA
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CLPGLACLRTSFNRFICLAOK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FEB-2002; 2002WO-JP000852.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-FEB-2001; 2001JP-00026820.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                 27-NOV-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                          WO200262944-A2.
                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                           15-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ohtaki T,
Hinuma S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19
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                                                                                                                                                  ABG94397;
61
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                                                                                                  ABG94397
                                                                                RESULT
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Length 108; Indels

100.0%; Score 461; DB 4; 100.0%; Pred. No. 4.3e-41; ive 0; Mismatches 0;

81; Conservative

Similarity

Local

Matches

8 g

Query Match

1 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP

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WPI; 2002-479752/51.
                                                                                                                                                                                                  Ehlert FJ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 108 AA;
                                                                                          WO200236625-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; ZVEN1;
         Homo sapiens.
                                                                                                                                                                                                                                                                                        constipation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               81;
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                                                                                                                10-MAY-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
                                                                                                                                                                                                  Zhou Q,
                                      Peptide
                                                            Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                           The invention comprises a method for producing an active peptide that has the same activity as a ZAQ ligand isolated from eukaryotic cells. The method of the invention is useful for the production of a physiologically active ZAQ ligand for use in preventing or treating digestive diseases (e.g. colitis and diarrhea). The present amino acid sequence represents a human physiologically active ZAQ ligand-related protein
                                                                                                                                                                                                                                                                                                                             Industrial production of physiologically-active ZAQ ligand by expressing in transformant prokaryote and refolding in redox buffer, for use in preventing or treating digestive diseases e.g. colitis and diarrhea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        87
                                                                                                    Human; ZAQ ligand; physiologically-active ZAQ ligand; digestive disease;
colitis; diarrhoea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPWGKLGDSCHPLTRKVPFFGRRMHHTCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; prokineticin 2; gastrointestinal motility; intestinal cancer; irritable bowel syndrome; gastrointestinal reflux disease; diarrhoea; diabetic gastroparesis; constipation; malabsorptive disorder; inflammatory bowel disorder; analgesic; infectious disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 461; DB 5; Length 108; llarity 100.0%; Pred. No. 4.3e-41; Conservative 0; Mismatches 0; Indels
                                                                                          Human physiologically-active ZAQ ligand-related protein 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human prokineticin 2 precursor protein.
                                                                                                                                                                                                                                                                                                                                                                         Disclosure, Page 88; 93pp; Japanese.
                                                                                                                                                                                                                                                                                      Nishimura O;
                             AAO15531 standard; protein; 108 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88 CLPGLACLRTSFNRFICLAQK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAE24384 standard; protein; 108 AA
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                                                                                                                                                                                                            21-JAN-2002; 2002WO-JP000378
                                                                                                                                                                                                                                22-JAN-2001; 2001JP-00013027
17-MAY-2001; 2001JP-00147759
                                                                                                                                                                                                                                                                 (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                      Suenaga M,
                                                                                                                                                                                                                                                                                                           WPI; 2002-566801/60.
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les 81; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 108 AA;
                                                                                                                                                                  WO200257443-A1
                                                                                                                                                Homo sapiens.
                                                                      24-OCT-2002
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                                                                                                                                                                                       25-JUL-2002
                                                                                                                                                                                                                                                                                      Yamada T,
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gastrointestinal smooth muscle contraction, useful for improving impaired gastrointestinal motility in irritable bowel syndrome, chronic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28 AVITGACDKDSQCGGGCCAVSIWVKSIRICTPWGKLGDSCHPLTRKVPFFGRRMHHTCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention relates to human prokineticin 1 and 2 polypeptides that
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                                                                                                                           /note= "Mature human prokineticin 2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             sequence is human prokineticin 2 precursor protein
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100.0%; Pred. No. 4.3e-41;
tive 0; Mismatches 0;
                                  1. .27
/label= Signal_peptide
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLPGLACLRISPNRFICLAOK 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 1; Fig 1; 86pp; English.
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                                                                                                                                                                                                                                                                                                                              01-NOV-2001; 2001WO-US047969
                                                                                                                                                                                                                                                                                                                                                                                           03-NOV-2000; 2000US-0245882P
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                                                                                        .108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            (REGC ) UNIV CALIFORNIA.
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US6485938-B1 26-NOV-2002

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The present invention relates to a novel method of inducing proliferation of endothelial cells or enhancing cell survival, involving contacting the cells with Bv8 or introducing a nucleic acid encoding Bv8 into the cells cells with Bv8 or introducing a nucleic acid encoding Bv8 into the cells to inducing proliferation or to enhance survival of the cells. The method is useful for inducing proliferation of endothelial cells and to enhance cell survival, where the cells are vascular endothelial cells and to enhance cell proliferation, for treating cancer (e.g., hormone-dependent cancer or cancer of the reproductive organs, especially testicular cancer) in cancer of the reproductive organs, especially testicular cancer) in the cancer of the reproductive organs, especially testicular cancer) in the condition associated with hormone producing tissue which is elected from lipoid congenital adrenal hyperplasia, infertility, sexual maturation, androgen-dependent tumours, precocious puberty, adrenal-chypoplasia congenita, McCune-Albright syndrome and hypogonadotropic hypogonadism. The present sequence is human Bv8 homologue splice variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inducing proliferation of endothelial cells or enhancing cell survival, by contacting the cells with Bv8 or introducing nucleic acid encoding Bv8 into cells to induce proliferation or to enhance survival of the cells.
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                                            22. .108
/note= "Human mature Bv8 homologue splice variant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%; Score 461; DB 6; Length 1
100.0%; Pred. No. 4.3e-41;
.ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                 "Myristoylation site"
                                                                                                                  41. .46
/note= "Myristoylation site"
42. .47
/note= "Myristoylation site"
                                                                                                                                                                                                                                                                             /note= "Amidation site"
. .21
label= Signal-peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                           27-AUG-2002; 2002WO-US027571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         29-AUG-2001; 2001US-0316184P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            81; Conservative
                                                                                        protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ferrara N, Le Couter J;
                                                                                                                                                                                                           .48
                                                                                                                                                                                                                                                       78. .81
                                                                                                                                                                                                                                 /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (GETH ) GENENTECH INC.
                                                                                                                                                                                                             43.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-290180/28.
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                                                                                                                  Modified-site
                                                                                                                                                            Modified-site
                                                                                                                                                                                                             Modified-site
                                                                                                                                                                                                                                                           Modified-site
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                                              Protein
  Peptide
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ADD69039
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to an isolated nucleic acid molecule (I) that encodes a Zveni polypeptide. (I) is useful for inhibiting the proliferation of tumour cells, as probes or primers to clone 5' non-coding regions of a Zven gene, to direct the expression of heterologous gene in tissues of, for example, transgenic animals or patients treated with gene therapy, to detect the expression of a Zveni or Zveni gene in a biological sample, to detect activated neutrophils, to identify the characteric agents that modulate the response of a neutrophil to a pathogen, to determine whether a subject's chromosomes contain a mutation in the Zven gene, or to detect aberrations in Zveni or Zveni journes in settle as educational tools, as laborations in Zveni chemistry and antibody production and analysis. The present sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bv8; androgen-dependent tumour; precocious puberty; sexual maturation; adrenal-hypoplasia congenita; infertility; hypogonadotropic hypogonadism; McCune-Albright syndrome; cytostatic; anglogenic; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP 60
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                                                                                                                                                                                                                                                                                                                                                                                                                        Novel isolated nucleic acid molecule that encodes a Zvenl polypeptide, useful for inhibiting the proliferation of tumor cells, or to detect the expression of a Zvenl or Zven2 gene in a biological sample.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 17; Col 3; 37pp; English
                                                                                                                                             16-NOV-1999; 99US-0165905P.
25-FEB-2000; 2000US-0184875P.
19-APR-2000; 2000US-019756P.
07-JUN-2000; 2000US-0210332P.
                                                                                                    14-NOV-2000; 2000US-00712529
                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB, ABX12102, ABX12103
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                                                                                                                                                                                                                                                                (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                               Sheppard PO, Bishop PD;
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Best Local Similarity
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Gaps

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Length 108;

9 87

ADD69039;

Location/Qualifiers

Synthetic

HX S S X K K K K K E X L X Y X Y X

Key

AAE36789;

RESULT 13

AAE36789

61

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human.

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The invention desribes an isolated Zvenl polypeptide comprising a sequence that is at least 70% identical to amino acid residues 23-108 of the 108-amino acid sequence and that binds with an antibody that specifically binds with a polypeptide comprising the sequence comprising 108 amino acids. The polypeptide has cytostatic properties and is useful in gene therapy. The protein is Zvenl procein and useful for preparing a composition for treating e.g. cancer. This sequence encodes the novel human polypeptide Zvenl encoded by a gene found on chromosome 3p21.1-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PROK1; PROK2; G protein-coupled receptor 192; GPCR 192; ligand; cancer; metabolic disorder; central nervous system disorder; gastrointestinal disorder; immune disorder; neuroprotective; immunosuppressive; cytostatic; agonist; entagonist.
                                                                                                                                                                                                                                                                       Zven1 protein, useful for preparing a composition for treating e.g.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 461; DB 7;
Pred. No. 4.3e-41;
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                                                                                                                                                                                                                                                                                                                              Claim 1; SEQ ID NO 2; 41pp; English
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                              16-NOV-1999; 99US-0165905P.
25-FEB-2000; 2000US-0184875P.
19-APR-2000; 2000US-019750P.
07-JUN-2000; 2000US-021332P.
14-NOV-2000; 2000US-00712529.
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02-AUG-2002; 2002US-00212201
                                                                                                                                                                                                                  WPI; 2003-897549/82.
N-PSDB; ADF28066, ADF28068.
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                                                                                                                                            (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                Bishop PD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 108 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WO2003083073-A2
                                                                                                                                                                              Sheppard PO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
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                                                                                                                                                                                                                                                                                              cancer
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a novel angiogenesis inhibitor comprising a compound that inhibits the activity of an amino acid sequence given in the specification. Angiogenesis-related proteins Bv8, ZAQ and ISE were utilised within the method of the invention. The molecules of the invention demonstrate cytostatic and antiinflammatory activities whilst the method may be useful for treatment and prevention of cancer, ovarian diseases, diabetic retinopathy and inflammatory disease. The current sequence is that of the human Bv8-related protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Zven1; cytostatic; gene therapy; cancer; human; chromosome 3p21.1-3p14.3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Angiogenesis inhibitors for treatment and prevention of cancer, ovarian diseases and inflammatory disease.
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                                                                                       angiogenesis inhibitor; cytostatic; antiinflammatory; cancer; ovarian disease; diabetic retinopathy; inflammatory; ZAQ; Bv8; ISE;
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; Pred. No. 4.3e-41;
0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 3; SEQ ID NO 17; 308pp; Japanese.
                                                   Human Bv8-related protein - SEQ ID 17.
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                                                                                                                                                                                                                                                                                                                                                                                     Takatsu Y;
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                  (first entry)
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Best Local Similarity 100...
Best Local 81; Conservative
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                                                                                                                                                                                                                                                                                                                                               (TAKE ) TAKEDA CHEM
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                                                                                                                                                                 Homo sapiens.
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RESULT 15 ADF28067 ADF28067;

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                                                                           Identifying an agonist or antagonist of G-protein-coupled-receptor 192, GPCR), useful for treating metabolic or immune disorders, or cancer comprises contacting GPCR 192 with a test compound, and detecting agonist or antagonist activity.
                                                                                                                                                                                             The present invention relates to a method of identifying an agonist or antagonist of G protein-coupled receptor (GPCR) 192, which comprises contacting GPCR 192 with a test compound, and detecting agonist or antagonist activity. The methods and compositions containing the agonist or antagonist are useful in the manufacture of a medicament for treating central inervous system, metabolic or immune disorders, or cancer. The present sequence is human prokinction 2 (PROK2) as shown in the exemplification of the invention
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                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 461; DB 7; Length 108; 100.0%; Pred. No. 4.3e-41;
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                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADJ71811 standard; protein; 108 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLPGLACLRTSFNRFICLAOK 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CLPGLACLRISFNRFICLAQK 81
                                                                                                                                                                  Claim 12; Fig 6; Opp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human prokineticin 2 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-NOV-2002; 2002WO-US035465
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                 81; Conservative
                            WPI; 2003-788345/74.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-441552/41
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Matches 81; Conserv
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                                               N-PSDB; ACH00975
                                                                                                                                                                                                                                                                                                                                                              Sequence 108 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 wounds; cancer.
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Gedrich R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADJ71811;
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                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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The invention relates to novel prokineticin-like polypeptides and polymucleotides. The polymucleotide and polypeptide are useful in diagnostics, forenists, gene mapping, drug screening, identification of diagnostics, forenists, gene mapping, drug screening, identification of mutations responsible for genetic disorders or traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences. The polymucleotide and products dependent on DNA and amino acid sequences. The polymucleotide and polypeptide may also be used for treating diseases due to impaired gastroparesis, irritable bowel syndrome or postoperational lleus), for regulating angiogenesis and neovascularization, as well as growth and development in heart and other tissues, for treating sperm disorders including accospermia, neurodegenerative diseases (e.g. Alzheimer's disease or Parkinson's disease), autoimmune disorders (e.g. rheumatoid arthritis, diabetes, allergy or asthmal), wounds, cancer or infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          human; Zven1; Zven2; prokineticin2; prokineticin1; G-protein coupled receptor; GPCR73a; GPCR73b; inflammation; intestine; inflammatory bowel disease; irritable bowel syndrome; ulcerative colitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                preventing or treating impaired gastrointestinal motility, cancer or neurodegenerative or autoimmune disorders, and for gene mapping or drug
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prokineticin-like polynucleotide and polypeptide for diagnosing,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Amino acid sequence of a human Zvenl polypeptide.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 461; DB 7;
100.0%; Pred. No. 4.3e-41;
iive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                 prokineticin-like proteins of the invention.
                                                                                        Disclosure, SEQ ID NO 17; 132pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADN41839 standard; protein; 108 AA
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07-OCT-2002; 2002US-0416719P.
16-DEC-2002; 2002US-0433918P.
16-DEC-2002; 2002US-0434116P.
03-OCT-2003; 2003US-0508603P.
03-OCT-2003; 2003US-0508614P.
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Best Local Similarity luv..
Local Similarity luv..
Local Similarity luv..
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                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 108 AA;
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Wood WI;

Schoenfeld J,

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Wu TD,
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Clark H,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81; Conservative
 Bodary S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human Zvenl protein.
                       2004-420080/39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                   N-PSDB; ADO24420
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 108 AA;
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  Abbas A,
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                                                                                                                                                  The present sequence represents a human Zven1 polypeptide. Zven1 and Zven2 are also known as prokineticin2 and prokineticin1, respectively. Receptors for Zven1 and Zven2 have been identified as G-protein coupled receptors, GPCR71a and GPCR71b. The specification describes a method for reducing or treating inflammation in the intestine of a mammal, comprising administering a Zven1 or Zven2 antagonist to reduce the inflammation in the intestine. The antagonist is preferably a receptor that binds Zven1 or Zven2. The method is useful for diagnosing or treating inflammatory bowel disease, irritable bowel syndrome, ulcerative colitis, or Crohn's disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRO; antianaemic; antiarthritic; antiinflammatory; antipsoriatic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 juvenile chronic arthritis, systemic lupus erythematosus;
spondyloarthropathy; systemic sclerosis;
ldiopathic inflammatory myopathy; Sjogren's syndrome;
systemic vasculitis; sarcolosis; autoimmune haemolytic anaemia;
autoimmune disease; immune-mediated skin disease; bullous skin disease;
                                                                                                                                                                                                                                                                                                                                                                      28 AVITGACDKDSQCGGGCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRM-HHTCP
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                                                                                Treating inflammatory bowel disease or irritable bowel syndrome in mammals comprises administering to the mammal a Zvenl or Zven2 polypeptide or nucleic acid molecule, or a Zvenl or Zven2 antagonist.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antirheumatic; dermatological; immunostimulant; immunosuppressive; osteopathic; vasotropic; immune related disease; inflammatory immune response; rheumatoid arthritis; osteoarthritis;
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                                                                                                                                                                                                                                                                                                            Length 108;
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                                                                                                                                                                                                                                                                                                            Score 461; DB 8;
Pred. No. 4.3e-41;
                                                                                                                                                                                                                                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human PRO28691 protein SEQ ID NO:60.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AD024421 standard; protein; 108 AA,
                                                                                                                                                                                                                                                                                                                                                                                                                       CLPGLACLRISFNRFICLAQK 108
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                                                                                                                                Claim 5; Page 3; 147pp; English
                                                                                                                                                                                                                                                                                                                                                                                                          61 CLPGLACLRISFNRFICLAQK
                                                                                                                                                                                                                                                                                                            100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           splenomegaly; leukopaenia.
                       Thompson PJ, Sheppard PO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                     Local Similarity 100.
 (ZYMO ) ZYMOGENETICS INC.
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                                              2004-340793/31.
                                                                                                                                                                                                                                                                                      Sequence 108 AA;
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                                                         N-PSDB; ADN41838
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens.
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                                                                                                                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 19
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The present invention describes an isolated human PRO polypeptide (1).

Also described: (1) an isolated PRO nucleic (II) acid encoding (I); (2) a vector (II) comprising (II); (3) a host cell (IV) comprising (II); (4) producing (I); (5) a chimeric molecule (V) comprising (II); (4) producing (I); (5) a chimeric molecule (V) comprising (II); (4) binds using (II); (7) a composition of matter comprising (I), an agonist of (I), an antagonist of (I), in combination with a carrier; (8) creating (MI) an immune related disease in a mammal, by administering (I), an agonist of (I), an antagonist of (I), or the antibody (VI); (9) diagnosing an immune related disease in a mammal, by detecting the level of expression of a gene encoding (I) in a test sample of tissue cells of expression of a gene encoding (I) in a test sample of tissue cells obtained from the mammal and in a control sample of known normal tissue cells of the same cell type; (10) identifying a compound that inhibits to the activity of (I); (II) identifying a compound that inhibits cent activity of (I); (II) identifying a compound that inhibits cent and (I); (II) identifying a compound that inhibits of mammal, by administering (I) or its antagonist to the mammal. (I) has antimanemic, antiarthritic, antiinflammatory, antipsoriatic, antiantendry immune telled disease in a mammal. (VI) is useful for diagnosing an inflammatory immune response in a mammal. (VI) are useful for the polypeptide. (MI) is useful for treating mammal having an immune content of surfamining the presence of (I) in a sample suspected of containing the surfamily artherity, invented and suspected of containing the surfamily artherity is useful for treating mammal having an immune surfamily and surfamily and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           dermatitis, psoriagis, lymphadenopathy, splenomegaly and leukopaenia. The present sequence represents a human PRO protein from the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                9
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gastric emptying; intestinal transit; gastroparesis; chemokine release;
neutrophil infiltration; appetite; weight gain; sensitization;
New isolated PRO polypeptide e.g. PRO37544, PRO69493, PRO87327 etc, capable of stimulating an immune response, useful for treating diseases such as rheumatoid arthritis, psoriasis, and leukopenia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      juvenile chronic arthritis, systemic lupus erythematosus, spondyloarthropathies, systemic sclerosis, idiopathic inflammatory myopathies, Sigeren's syntemic vasculitis, sarcoidosis, autoimmume haemolytic anaemia, autoimmume or immune-mediated skin diseases including bullous skin diseases, erythema multiforme and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                .;
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                                                                                                                                                                                                                         Claim 9; SEQ ID NO 60; 326pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADS86957 standard; protein; 108 AA
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Antinflammatory; Gaetrointestinal; Neuroprotective; Muscular;
Antipsoriatic; Antiathritic; Antirheumatic; Antithyroid; Hepatotropic;
Virucide; Antidiabetic; Antianemic; haematopoiesis; autoimmune disorder;
Virucide; Antidiabetic; Antianemic; haematopoiesis; autoimmune disorder;
Bv8; Endocrine Gland derived Vascular Endochelial Growth Factor; EG-VEGF;
hematological disorder; leukaemia; myeloproliferative disorder;
Imphodysplastic disorder; lymphoproliferative disorder;
Immphodysplastic disorder; lymmunodeficiency disorder; HIV infection;
neutropenia; bacterial infection; lymphopaenia; autoimmune disorder;
multiple solerosis; myssthenia gravis; optic neuritis; lupus;
multiple solerosis; myssthenia gravis; optic neuritis; psoriasis;
rheumatoid arthritis; Graves Disease; autoimmune hepatitis;

type I diabetes; aplastic anaemia; human.

WO2004081229-A2 23-SEP-2004.

12-MAR-2003; 2003US-0454462P. 14-OCT-2003; 2003US-0511390P. 12-MAR-2004; 2004WO-US007622.

Ferrara N, Lecouter J; (GETH) GENENTECH INC.

WPI; 2004-690608/67.

N-PSDB; ADS00459.

Cytostatic; Antimicrobial; Anti-HIV; Immunostimulant; Antibacterial;

Human Bv8 homologue variant #2, SEQ ID 4.

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The invention relates to the used of a polypeptide for modulating contractility, gastric emptying or intestinal transit in a mammal, treating gastroparesis, stimulating chemokine release, stimulating neutrophil infiltration, inducing or increasing appetite or estimulating neutrophil infiltration, inducing or increasing appetite or weight gain in a mammal, increasing or decreasing sensitization to a thermal, mechanical or painful stimulus in a mammal, or inducing thermal, mechanical or painful stimulus in a mammal, or inducing or and polymucleotides are useful for treating intestinal motility disorders and improving gastrointestinal function with Zvenl and Zven2 and improving gastrointestinal function with Zvenl and Zven2 contractility, gastric emptying or intestinal transit in a mammal, contractility, stimulating gastrointestinal contractility, stimulating chemokine cappetite or weight gain in a mammal, increasing or increasing cappetite or weight gain in a mammal, increasing or decreasing mammal, cappetite or weight gain in a mammal, increasing or decreasing cappetite or weight gain in a mammal, increasing or decreasing cappetite or weight gain in a mammal, increasing or decreasing or increasing cannique and mammal, mechanical or painful stimulating mammal, continulating vasculogenesis or anglogenesis in cardiac stem cells. This cappeting contraction to the human Zvenl protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                thermal stimulus; mechanical stimulus; painful stimulus; vasculogenesis; angiogenesis; zvenl; zvenl; zvenl; zvenl; zvenl;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Use of Zvenl and Zven2 polypeptides for modulating gastrointestinal contractility, gastric emptying or intestinal transit in a mammal, stimulating gastrointestinal contractility, or for treating gastroparesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 108;
                                                                                                                                                                                                                                                                                                                                                                                                     West RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 461; DB 8; 100.0%; Pred. No. 4.3e-41;
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                                                                                                                                                                                                                                                                                                                                                                                                     Jaspers SR, Garcia RM,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 2; 143pp; English.
                                                                                                                                                                                                                  2002US-0416718P.
2002US-0416719P.
2002US-0433918P.
2002US-0434116P.
2003US-00416718.
                                                                                                                                                                               07-OCT-2003; 2003WO-US031714.
                                                                                                                                                                                                                                                                                                                       03-OCT-2003; 2003US-00416719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity 100.
nes 81; Conservative
                                                                                                                                                                                                                                                                                                                                                              (ZYMO ) ZYMOGENETICS INC
                                                                                                                                                                                                                                                                                                                                                                                                     Lewis KE,
Chan C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             2004-330174/30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; ADS86956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 108 AA;
                                                                                                   WO2004031367-A2.
                                                                                                                                                                                                                                                                                                                                                                                                     Thompson PJ,
Holderman SD,
                                                               Homo sapiens.
                                                                                                                                                                                                                                                             16-DEC-2002;
                                                                                                                                                                                                                                                                              16-DEC-2002;
                                                                                                                                                                                                                      07-OCT-2002;
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                                                                                                                                                                                                                                                                                                     03-OCT-2003;
                                                                                                                                          15-APR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
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The present invention relates to a method (M1) for treating a disorder associated with abnormal haematopoiesis or an autoimmune disorder in a mammal. The method comprises administering antagonists for BVB or Endocrine Gland derived Vascular Endothélial Growth Factor (EG-VEGF) to the mammal. BVB and EG-VEGF are honologies of Vascular Endothelial Growth Factor (EG-VEGF) to the mammal. BVB and EG-VEGF are honologies of Vascular Endothelial Growth Factor (WEGF), an angiogenic factor known to have an important role in the manural growth and survival. (M1) is useful for treating abnormal content of growth and survival. (M1) is useful for treating abnormal content is acute myelopicliferative disorder, myelodysplastic disorder. The leukaemia is acute myeloid leukaemia. (M1) is useful for treating immunodeficiency disorder and so primary immunodeficiency disorder. Blymphocyte disorder, growth and sprimary immunodeficiency disorder. I lymphocyte disorder such as primary immunodeficiency disorder. Blymphocyte condition associated with an infectious disease (HIV infection). The immunodeficiency disorder is a condition associated with an infectious disease. Condition associated with an infectious disease. Condition, associated with an infectious disease. Condition, upus, multiple salences. The vesting lymphopaenia or colitis, lugus, multiple salences, mysathenia gravis, optic neuritis, colitis, lugus, multiple salences, mysathenia gravis, optic neuritis, colitis, lugus, multiple salences, mysathenia gravis, optic neuritis, sequence used to illustrate the method of the invention. The present sequence coding sequences for human Bv8 due to alternative septions. The present sequence coding sequences for human Bv8 due to alternative septions. The present sequence concluded to a promptise the method of the invention. The present sequence concluder and promptise the hoparin binding domain. The present sequence concluded to a promptise of the method of the invention of the promptise of the present sequence concluded to a promptise 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treating disorder associated with abnormal hematopoiesis or autoimmune disorder by administering antagonist of small protein obtained from Bombina variegata or endocrine gland derived vascular endothelial growth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 52; SEQ ID NO 4; 161pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             factor, to mammal.
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Sequence 108 AA;

ADS00460 standard; protein; 108 AA.

RESULT 21

16-DEC-2004 (first entry)

ADS00460;

SXE

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Gaps

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Indels

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Mismatches

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81; Conservative

Matches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                human; Zven1; Zven2; prokineticin2; prokineticin1;
G-protein coupled receptor; GPCR73a; GPCR73b; inflammation; intestine;
inflammatory bowel disease; irritable bowel syndrome; ulcerative colitis;
                                                                                                                                       9
                                                                                                                                                                1 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP
                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Amino acid sequence of a human Zvenl with Glu-Glu tag and Gly linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mammals comprises administering to the mammal a Zven1 or Zven2
polypeptide or nucleic acid molecule, or a Zven1 or Zven2 antagonist
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Treating inflammatory bowel disease or irritable bowel syndrome in
                                                                              ;
0
               Length 108;
                                                                        Indels
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0
            ; Score 461; DB 8;
; Pred. No. 4.3e-41;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                          CLPGLACLRTSFNRFICLAQK 108
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                                                                                                                                                                                                                                                        61 CLPGLACLRTSFNRFICLAQK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADN41861 standard; protein; 116
               100.0%;
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2002US-0433918P.
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2003US-0508603P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
Query Match
Best Local Similarity 100.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (ZYMO ) ZYMOGENETICS INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thompson PJ, Sheppard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2004-340793/31.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-PSDB; ADN41860.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004032850-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Crohn's disease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-OCT-2002; 2
07-OCT-2002; 2
16-DEC-2002; 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Homo sapiens.
Synthetic.
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03-OCT-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                           ADN 1861
ADDN 1861
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Score 461; DB 8; Length 116; Pred. No. 4.6e-41;

100.0%;

Query Match Best Local Similarity

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The invention relates to the used of a polypeptide for modulating gastrointestinal contractility, gastric emptying or intestinal transit in a mammal, treating gastropatesis, stimulating chemokine release, stimulating neutrophil infiltration, inducing or increasing appetite or stimulating neutrophil infiltration, inducing or increasing appetite or weight gain in a mammal, increasing or decreasing sensitization to a thermal, mechanical or painful stimulus in a mammal, or inducing thermal, mechanical or painful stimulus in a mammal, increasing intestinal motility disorders and improving gastrointestinal function with Zvenl and Zven2 and improving gastrointestinal function with Zvenl and Zven2 and improving gastrointestinal function with zvenl and zven2 contractility, gastric emptying or increating intending gastrointestinal contractility, stimulating gastrointestinal contractility, stimulating chemokine release, stimulating neutrophil infiltration, inducing or increasing cappetite or weight gain in a mammal, increasing or decreasing sensitization to a thermal, mechanical or painful stimulus in a mammal, contractility creating to a captric entraction to a thermal, mechanical or painful stimulus in a mammal, or inducing vasculogenesis or anglogenesis in cardiac stem cells. This
9
                                   87
                                                                                                                                                                                                                                                                                                                                                                              gastrointestinal; anabolic; gastrointestinal contractility; gastroic emptying; intestinal transit; gastroparesis; chemokine release; neutrophil infiltration; appetite; weight gain, sensitization; thermal stimulus; mechanical stimulus; painful stimulus; vasculogenesis; angiogenesis; cardiac stem cell; motility disorder; Zven1; Zven2.
  1 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP
                      28 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMFHTCP
                                                                                                                                                                                                                                                                                                                                         Human Zvenl protein expressed in baculovirus cell expression system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Use of Zven1 and Zven2 polypeptides for modulating gastrointestinal contractility, gastric emptying or intestinal transit in a mammal, stimulating gastrointestinal contractility, or for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            West RR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Jaspers SR, Garcia RM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 9; SEQ ID NO 26; 143pp; English.
                                                                                                   CLPGLACLRISFNRFICLAQK 108
                                                                                                                                                                                                                       ADS86981 standard; protein; 116 AA.
                                                                              61 CLPGLACLRISFNRFICLAQK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2002US-0416718P.
2002US-0416719P.
2002US-0433918P.
2002US-0434116P.
2003US-00416718.
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                                                                                                                                                                                                                                                                                                    (first entry)
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Chan C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2004-330174/30.
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Holderman SD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens
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16-DEC-2002;
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03-OCT-2003;
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                                                                                                                                                                                                                                                            ADS86981;
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                                                                                                                                                                                  RESULT 23
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Indels

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Pred. No. 1.1e-40; Mismatches

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80; Conservative
Best Local Similarity
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                                                                                                                                                                                                        ADD69044;
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                                                                                      61
                                                                                                              19
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             Matches
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                                                                                                                                                      RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                  antiinflammatory; antidiarrhoeic; neuroleptic; neuroprotective; receptor.
                                                                                                               1 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP 60
                                                                                                                                          87
                                                                                                                                                                                                                                                                                                                                                                G-protein coupled receptor; GPCR; ZAQ; human; ZAQC; ZAQT; rat; ZAQ1; rZAQ1; rZAQ2; mouse; 15E receptor; m15E; GPR73; Bv8 protein; MIT1; digestive disorder; central nervous system disorder; CNS; diarrhoea; bowel inflammation; constipation; food absorption disorder; nootropic; Alzheimer's disease; Parkinson's disease; schizophrenia; laxative;
                                                                                                                                 28 AVITGACDKDSQCGGGCACCAVSIWVKSIRICTPWGKLGDSCHPLTRKVPFFGRRWHHTCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Screening of compounds modifying the binding of G-protein coupled receptor protein ZAQ and related proteins to their ligands for use in treatment and diagnosis of digestive disorders.
                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Shintani
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  sequence corresponds to the human Zvenl protein expressed in baculovirus cell expression system.
                                                                 Length 116;
                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Terao Y,
                                                                                                                                                                                                                                                                                                                                       C-terminal Lys truncated human GPCR ligand Bv8 protein.
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                                                                            4.6e-41;
                                                               100.0%; Score 461; DB 8;
100.0%; Pred. No. 4.6e-41;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Page 166-167; 197pp; Japanese.
                                                                                                                                                                                     81
                                                                                                                                                                                                                                                               ABG94400 standard; protein; 80 AA.
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                                                                                                                                                                      61 CLPGLACLRTSFNRFICLAOK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-FEB-2001; 2001JP-00026820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (TAKE ) TAKEDA CHEM IND LTD
                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                          81; Conservative
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S;
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                                                               Query Match
Best Local Similarity
Matches 81; Conserv
                                         Sequence 116 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens.
                                                                                                                                                                                                                                                                                                                  27-NOV-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Angiogenesis inhibitors for treatment and prevention of cancer, ovarian diseases and inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP
                                                                                                             AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           angiogenesis inhibitor; cytostatic; antiinflammatory; cancer; ovarian disease; diabetic retinopathy; inflammatory; ZAQ; Bv8; I5E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Example 3; SEQ ID NO 22; 308pp; Japanesd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human Bv8-related protein - SEQ ID 22.
                                                                                                                                                                                                                                                                                                                                                      ADD69044 standard; protein; 80 AA.
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100.0%; Pri
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                                                                                                                                                                                  CLPGLACLRTSFNRFICLAQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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RESULT 26

Length 80;

DB 5;

Score 456;

98.98;

Query Match

us-10-811-328-6.rag

ABG94402

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Rat, rZAQ1; rZAQ2; G protein-coupled receptor; GPCR; antidiarrheic; laxative; drug development; digestive organ disease; colitis; diarrhoea; constipation; malabsorption syndrome; diagnosis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human and rat brain-originated G protein-coupled receptor proteins and encoded DNAs, for developing drugs to treat diseases of the digestive organs, e.g. colitis, diarrhea, constipation and mal-absorption syndrome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention describes human and rat brain-originated G protein-coupled receptor (GPCR) proteins. The GPCR sequences have antidiarrheic and laxative activities. The GPCR sequences can be used for developing drugs to treat diseases of the digestive organs, e.g. colitis, diarrhoea, constibation and malabsorption syndrome, including gene diagnosis and therapy. The present sequence represents a rat GPCR protein sequence, which is used in an example from the present invention
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                                     protein-coupled receptor protein sequence SEQ ID NO:71.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 445; DB 5; I
Pred. No. 1.6e-39;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 5; Page 128; 135pp; Japanese.
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95.1%;
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19-JUN-2002 (first entry)
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N-PSDB; ABL50715.
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                                                                                                                                                                                                             WO200216607-A1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
                                                                                                                                                                                                                                                                                               antiinflammatory; antidiarrhoeic; neuroleptic; neuroprotective; receptor,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
                                                                                                                                                                                   G-protein coupled receptor; GPCR; ZAQ; human; ZAQC; ZAQT; rat, ZAQ1, rZAQ1; rZAQ2; mouse; ISE receptor; mISE; GRR73; Bv8 protein; MIT1; digestive discorder; central nervous system disorder. CNS; disarrhoes; bowel inflammation; constipation; food absorption disorder; nootropic; Alzheimer's disease; Parkinson's disease; schizophrenia; laxative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Screening of compounds modifying the binding of G-protein coupled receptor protein ZAQ and related proteins to their ligands for use in treatment and diagnosis of digestive disorders.
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0
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Pred. No. 1.6e-39;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 5; Page 173-174; 197pp; Japanese.
                                                                                                                                           Rat GPCR ligand Bv8 protein sequence #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ABB06963 standard; protein; 81 AA.
                 ABG94402 standard; protein; 81 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Takatsu Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLPGLACLRTSFNRFICLARK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CLPGLACLRTSFNRFICLAQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-2002; 2002WO-JP000852.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           96.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             02-FEB-2001; 2001JP-00026820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (TAKE ) TAKEDA CHEM IND LTD
                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 95.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Masuda Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2002-627537/67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-PSDB; ABS71120.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 81 AA;
                                                                                                                                                                                                                                                                                                                                                                               WO200262944-A2
                                                                                                     27-NOV-2002
                                                                                                                                                                                                                                                                                                                                                                                                                         15-AUG-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ohtaki T,
Hinuma S;
                                                                                                                                                                                                                                                                                                                                         Rattus sp
                                                             ABG94402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ABB06963;
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Matches

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ABB06963

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Gaps ö

Indels

81;

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The invention relates to a method of screening for a compound for its ability to modulate circadian rhythm. The method involved determining the ability to modulate circadian rhythm. The method involved determining the ability of a prokinctichi 2 (PKZ) receptor agonist or antegonist to modulate one or more indicia or circadian rhythm function. The compound ce determining its effect on a predetermined signal such as calcium mobilisation produced by the interaction of FkZ and a receptor selected from the PkZ receptor (e.g., ADO05353) or the PkI receptor (e.g., ADO05355). The invention is based on the findings that PkZ expression in the receptor activation modulates circadian fashion, and that PkZ receptor activation modulates circadian rhythm of an animal by administration of a PkZ receptor antagonist; a composition comprising a detectably labelled PkZ and an isolated mouse composition comprising a detectably labelled PkZ and an isolated mouse composition comprising a detectably labelled PkZ and an isolated mouse composition comprising a detectably labelled PkZ and an isolated mouse composition romprising a detectably labelled PkZ and an isolated mouse composition comprising a detectably labelled PkZ and an isolated mouse composition nucleoid sequence; use of such constructs to identify modulators of circadian rhythm and for the light regulated expression of a nucleic acid contour an animal, and oligonucleotides at least 17 bases in length comprising circadian rhythm; such modulators include PkZ promoter ADO05365. The modulators include PkZ promoter ADO05365. The composition which are able to hybridise to the human PkZ promoter ADO05365. The contour of the label and an animal a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antagonists which promote sleep, and PKZ receptor agonists which promote alertness. The circadian rhythm modulators may be used in the treatment of circadian rhythm disorders such as non-24-hour sleep-wake syndrome, rapid time-zone change syndrome (jetlag), work-shift syndrome, grandrome, advanced sleep phase syndrome, irregular sleep-wake pattern syndrome, syndrome associated with decreased amplitude, and seasonal affective disorder. They may also be used for modulating biological rhythms with a periodicity of less than 24 hours (ultradian rhythm) such as daydreaming, unination or hunger, or those with a periodicity of more than 24 hours (infardian rhythm) such as sexual receptivity (heat) in female animals. The present sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neurogenesis, prokineticin receptor; PKR; neural stem; progenitor cell; neural regeneration; Alzheimer's disease; Parkinson's disease; neurodegenerative disease; prokineticin 2; PK2.
                                                                    seasonal disorders, comprises determining ability of prokineticin-2 receptor antagonist or agonist to modulate one or more circadian rhythm function indicia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP
                                                       compounds for modulating circadian rhythm, for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 445; DB 7; Length 81; Pred. No. 1.6e-39; 4; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of murine prokineticin 2 (PK2).
                                                                                                                                                                Disclosure; SEQ ID NO 7; 164pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       81
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                WPI; 2003-854028/79.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      major murine PK2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 81 AA;
                                                           Screening for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        15-JUL-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mouse; murine; prokineticin 2; PK2; circadian rhythm; modulation; drug screening; circadian rhythm disorder; non-24-hour sleep-wake syndrome; rapid time-zone change syndrome; jetlag; work-shift syndrome; delayed phase sleep syndrome; advanced sleep phase syndrome; irregular sleep-wake pattern syndrome; decreased amplitude syndrome; seasonal affective disorder; ultradian rhythm; daydreaming; urination; hunger; infardian rhythm; female sexual receptivity; CNS; central nervous syndrome;
                                                                                                                                                                                                                                                                                                                                            The invention relates to a novel angiogenesis inhibitor comprising a compound that inhibits the activity of an amino acid sequence given in the specification. Angiogenesis-related proteins Bv8, ZAQ and ISE were utilised within the method of the invention. The molecules of the invention demonstrate cytostatic and antiinflammatory activities whilst the method may be useful for treatment and prevention of cancer, ovarian diseases, diabetic retinopathy and inflammatory disease. The current sequence is that of the rat Bv8-related protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
                                                                                                                                                                                                                                          Angiogenesis inhibitors for treatment and prevention of cancer, ovarian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AVITGACDKDSQCGGGMCCAVSIWIKTPMGKLGDSCHPLTRKVPFFGRRMHHTCP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ;
0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              96.5%; Score 445; DB 7; L. 95.1%; Pred. No. 1.6e-39; ive 4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse major prokineticin 2 (PK2), SEQ ID NO:7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PK2 receptor antagonist; PK2 receptor agonist
                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 39; 308pp; Japanese.
                                                                                                                                                                                                                                                                 diseases and inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLPGLACLRISFNRFICLAOK 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADO05358 standard; protein; 81
                                                                                                                                  Takateu
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03-FEB-2003; 2003WO-JP001057
                                             04-FEB-2002; 2002JP-00027299
                                                                                       (TAKE ) TAKEDA CHEM IND LID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                              Ohtaki T, Masuda Y,
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                                                                                                                                                                         WPI; 2003-646310/61.
                                                                                                                                                                                                   N-PSDB; ADD69062
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 81 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Matches
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Takatsu Y,
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                                                                                                                                                                                                                                                                                                                 96.5%;
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04-OCT-2002; 2002US-0416202P.
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                                                                                                                                                                                                                                                                                                                                      77; Conservative
                     (REGC ) UNIV CALIFORNIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Masuda Y,
                                                              WPI; 2004-340794/31.
                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                          Cheng MY;
                                                                                                                                                                                                                                                                                             Sequence 81 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200262944-A2
                                                                                                                    neurogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          27-NOV-2002
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Hinuma S;
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                                          Zhou Q,
                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                         The specification describes a method for identifying a compound that modulates neurogenesis. The method comprises providing a compound that modulates prokineticin receptor (PKR) signaling, contacting a neural stem or progenitor cell with the compound, and determining the ability of the compound to modulate neurogenesis. The method is useful for modulating neurogenesis or for identifying compounds that modulate neurogenesis. These are used for both ex vivo or in vivo therapeutic applications where neural regeneration is desirable, such as in Alzheimer's disease, parkineno's disease or other debilitating neurodespenerative diseases. The used in the method of the invention to modulate neurogenesis.
                                                                                                                                                                                    Identifying a compound that modulates neurogenesis comprises contacting a
                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  neurogenesis; prokineticin receptor; PKR; neural stem; progenitor cell; neural regeneration; Alzheimer's disease; Parkinson's disease; neurodegenerative disease; prokineticin 2; PK2.
                                                                                                                                                                                              neural stem or progenitor cell with a compound that modulates
prokineticin receptor signaling and determining its ability to modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AVITGACDKDSQCGGGMCCAVSIWKSIRICTPMGQVGDSCHPLTRKVPFWGRRMHHTCP
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                                                                                                                                                                                                                                                                                                                                                                                                                 Length 81;
                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Amino acid sequence of rat prokineticin 2 (PK2)
                                                                                                                                                                                                                                                                                                                                                                                                                 96.5%; Score 445; DB 8; 95.1%; Pred. No. 1.6e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61 CLPGLACLRTSFNRFICLAQK 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ADN43262 standard; protein; 81 AA
                                                                                                                                                                                                                                        Claim 26; Fig 6B; 103pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLPGLACLRISFNRFICLARK
                                                                         03-OCT-2003; 2003WO-US031626
                                                                                             04-OCT-2002; 2002US-0416202P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                   (REGC ) UNIV CALIFORNIA
                                                                                                                                                               WPI; 2004-340794/31
                                                                                                                                         Cheng MY;
                              WO2004032851-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO2004032851-A2.
                                                                                                                                                                                                                                                                                                                                                                                            Sequence 81 AA;
                                                                                                                                                                                                                    neurogenesis.
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                                                     22-APR-2004
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                                                                                                                                         Zhou Q,
           Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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The specification describes a method for identifying a compound that modulates neurogenesis. The method comprises providing a compound that modulates prokineticin receptor (PKR) signaling, contacting a neural stem modulates prokineticin receptor (PKR) signaling, contacting a neural stem or progenitor cell with the compound, and determining the ability of the compound to modulate neurogenesis. The method is useful for modulating neurogenesis or for identifying compounds that modulate neurogenesis. These are used for both ex vivo or in vivo therapeutic applications where neural regeneration is desirable, such as in Alzheimer's disease, parkinson's disease or other debilitating neurodegenerative disease. The present sequence represents rat prokineticin 2 (PK2), which may be used in the method of the invention to modulate neurogenesis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antiinflammatory, antidiarrhoeic, neuroleptic, neuroprotective, receptor.
Identifying a compound that modulates neurogenesis comprises contacting neural stem or progenitor cell with a compound that modulates prokineticin receptor signaling and determining its ability to modulate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     G-protein coupled receptor; GPCR; ZAQ; human; ZAQC; ZAQT; rat; ZAQ1; rZAQ1; rZAQ2; mouse; ISE receptor; mISE; GPR73; Bv8 protein; MIT1; disentive discorder; central nervous system disorder; CNS; diarrhoea; bowel inflammation; constigation; food absorption disorder; nootropic; Alzheimer's disease; parkinson's disease; schizophrenia; laxative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 81;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 445; DB 8;
Pred. No. 1.6e-39;
4; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Watanabe T,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81
                                                                                                                                                                                                                    Claim 26; Fig 6B; 103pp; English
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                                                                                                                                                      The present invention relates to a screening method for compounds for their ability to modify the binding of G-protein coupled receptor (GPCR) protein ZAQ2 and related proteins (human ZAQ2, rat ZAQ1 (rZAQ1), rZAQ2, human and mouse ISE (MISB) receptor, and mouse GPR73 to their ligands (the mature form of human, mouse or rat Bv8 protein). The receptor protein and ligand are contacted in the presence or absence of the test compound. The compounds are useful in a drug composition for the treatment, and prevention of digestive and central nervous system (CNS) disorders, including bowel inflammation, diarrhoea, constipation, food absorption disorders, Altheimer's disease, Parkinson's disease and
                                                                                                                                                                                                                                                                                                                                                                                                                                                             9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiinflammatory; antidiarrhoeic; neuroleptic; neuroprotective; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86
                                                                                                                                                                                                                                                                                                                             schizophrenia. The present sequence represents a GPCR or related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               G-protein coupled receptor; GPCR; ZAQ; human; ZAQC; ZAQT; rat; ZAQ1; rZAQ1; rZAQ2; mouse; ISE receptor; mISE; GPR73; Bv8 protein; MIT1; digestive disorder; central nervous system disorder; CNS; diarrhoea; bowel inflammation; constipation; food absorption disorder; nootropic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPWGQVGDSCHPLTRKVPFWGRRMHHTCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP
                                                        Screening of compounds modifying the binding of G-protein coupled receptor protein ZAQ and related proteins to their ligands for use in treatment and diagnosis of digestive disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Terao Y, Shintani Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alzheimer's disease; Parkinson's disease; schizophrenia; laxative;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Screening of compounds modifying the binding of G-protein coupled
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0
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Hinuma S;
                                                                                                                                                                                                                                                                                                                                                                                              Score 445; DB 5;
Pred. No. 2.1e-39;
4; Mismatches 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rat GPCR ligand Bv8 protein sequence #1.
                                                                                                                            Disclosure; Page 189; 197pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABG94401 standard; protein; 107 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLPGLACLRTSFNRFICLARK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLPGLACLRTSFNRFICLAQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02-FEB-2001; 2001JP-00026820.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-2002; 2002WO-JP000852
                                                                                                                                                                                                                                                                                                                                                                                                96.5%;
95.1%;
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                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 95.1.
Local 77; Conservative
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             WPI; 2002-627537/67.
N-PSDB; ABS71130.
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                                                                                                                                                                                                                                                                                                                                                                 Sequence 107 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABG94401;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 33
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                                                                                The present invention relates to a screening method for compounds for their ability to modify the binding of G-protein coupled receptor (GPCR) protein ZAQ and related proteins (human ZAQC, human ZAQC, rat ZAQQ. (YZAQQ), raZAQQ, human and mouse ISE (MISE) receptor, and mouse GPR73) to receptor protein and ligand are contacted in the presence or absence of the test compound. The compounds are useful in a drug composition for the treatment, and prevention of digestive and central nervous system (CNS) disorders, including bowel inflammation, diarrhoea, constipation, food absorption disorders, Alzheimer's disease, Parkinson's disease and schizophrenia. The present sequence represents a GPCR or related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes human and rat brain-originated G protein-coupled receptor (GPCR) proteins. The GPCR sequences have antidiarrheic and laxative activities. The GPCR sequences can be used for developing drugs to treat diseases of the digestive organs, e.g. colitis, diarrhoea
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human and rat brain-originated G proteif-coupled receptor proteins and encoded DNAs, for developing drugs to treat diseases of the digestive organs, e.g. colitis, diarrhea, constipation and mal-absorption syndrome
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rat; rZAQ1; rZAQ2; G protein-coupled receptor; GPCR; antidiarrheic; laxative; drug development; digestive organ disease; colitis; diarrhoea; constipation; malabsorption syndrome; diagnosis; gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP
 ä
                                                                                                                                                                                                                                                                                                                                                                                  Gaps
receptor protein ZAQ and related proteins to their ligands for use treatment and diagnosis of digestive disorders.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rat G protein-coupled receptor protein sequence SEQ ID NO:69.
                                                                                                                                                                                                                                                                                                                                           Score 445; DB 5; Length 107; Pred. No. 2.18-39; 4; Mismatches 0; Indels
                                                        Page 172-173; 197pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 5; Page 127; 135pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABB06962 standard; protein; 107 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLPGLACLRISFNRFICLARK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 61 CLPGLACLRTSFNRFICLAQK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23-AUG-2001; 2001WO-JP007209.
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                                                                                                                                                                                                                                                                                                                                                  96.5%;
                                                                                                                                                                                                                                                                                                                                                                   95.1%;
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Matches 77; Conservative
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                                                                                                                                                                                                                                                                                                               Sequence 107 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ABB06962;
                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                        Claim
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                                                                                                                                                                                                                                                                                                                                                                                               Mouse; cell proliferation, cancer; lipoid congenital adrenal hyperplasia; Bv8; androgen-dependent tumour; precocious puberty; sexual maturation; adrenal-hypoplasia congenita; infertility; hypogonadotropic hypogonadism; McCune-Albright syndrome; cytostatic; angiogenic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a novel method of inducing proliferation of endothelial cells or enhancing cell survival, involving contacting the
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                                                                                                                                                    27 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPWGQVGDSCHPLTRKVPFWGRRMHHTCP
constipation and malabsorption syndrome, including gene diagnosis and therapy. The present sequence represents a rat GPCR protein sequence, which is used in an example from the present invention
                                                                                                                                      1 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP
                                                                                                            Gaps
                                                                                                           ;
0
                                                                                Length 107;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Mouse mature Bv8 homologue protein"
                                                                                                         Indels
                                                                                Score 445; DB 5; Le
Pred. No. 2.1e-39;
4; Mismatches 0;
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te= "Myristoylation site"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Amidation site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. .20
/label= Signal-peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                       AAE36790 standard; protein; 107 AA
                                                                                                                                                                                                                   CLPGLACLRISFNRFICLARK 107
                                                                                                                                                                                          61 CLPGLACLRTSFNRFICLAQK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 9; Fig 6; 87pp; English
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                                                                                96.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-AUG-2001; 2001US-0316184P.
                                                                                                                                                                                                                                                                                                                                                                      Mouse Bv8 homologue protein.
                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                             Local Similarity 95.1
les 77; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     .107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (GETH ) GENENTECH INC
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N-PSDB; AAD55708.
                                                       Sequence 107 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mus musculus.
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                                                                                Query Match
                                                                                                                                                                                                                                                                                                                  AAE36790;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein
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                                                                                                                                                                                                                                                             RESULT 35
                                                                                                                                                                                                                                                                       AAE36790
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cells with Bv8 or introducing a nucleic acid encoding Bv8 into the cells to induce proliferation or to enhance survival of the cells. The method is useful for inducing proliferation of endothelial cells and to enhance cell survival, where the cells are vascular endothelial cells, especially steroidogenic endothelial cells. It is useful for inhibiting endothelial cell proliferation, for treating cancer (e.g., hormone-dependent cancer or cancer of the reproductive organs, especially testicular cancer) in mammals preferably human. The method of the invention is also useful for treating a condition associated with hormone producing tissue in mammals, where the condition is associated with hormone producing tissue which is selected from liboid congenital adrenal hyperplasia, infertility, sexual maturation, andregen-dependent tumnurs, precocious puberty, adrenal hypoplasia congenita, McCune-Albright syndrome and hypogonadorropic hypogonadism. The present sequence is mouse Bv8 homologue protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel angiogenesis inhibitor comprising a compound that inhibits the activity of an amino acid sequence given in the specification. Angiogenesis-related proteins Bv8, ZAQ and ISE were utilised within the method of the invention. The molecules of the invention demonstrate cytostatic and antiinflammatory activities whilst the method may be useful for treatment and prevention of cancer, ovarian diseases, diabetic retinopathy and inflammatory disease. The current sequence is that of the rat Bv8-related protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                              98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         angiogenesis inhibitor; cytostatic; antiinflammatory; cancer; ovarian disease; diabetic retinopathy; inflammatory; ZAQ; Bv8; I5E; rat.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Angiogenesis inhibitors for treatment and prevention of cancer, ovarian diseases and inflammatory disease.
                                                                                                                                                                                                                                                                                                                                                                                                                              1 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP
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                                                                                                                                                                                                                                                                                                                               Length 107;
                                                                                                                                                                                                                                                                                                                                 Score 445; DB 6;
Pred. No. 2.1e-39;
                                                                                                                                                                                                                                                                                                                 96.5%; Scc. No. 2.2
95.1%; Pred. No. 2.2
... 4; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bv8-related protein - SEQ ID 37
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADD69059 standard; protein; 107 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLPGLACLRISFNRFICLARK
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                                                                                                                                                                                                                                                                                                                                                                       77; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-646310/61.
                                                                                                                                                                                                                                                                                                                                                   Local Similarity
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                                                                                                                                                                                                                                                                                            Sequence 107 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rattus sp.
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                                                                                                                                                                                                                                                                                                                                 Query Match
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                                                                                   9
                                                                                                27 AVITGACDKDSQCGGGCACAVSIWVKSIRICTPMGQVGDSCHPLTRKVPFWGRRWHHTCP 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Angiogenesis inhibitors for treatment and prevention of cancer, ovarian diseases and inflammatory disease.
                                                                                   1 AVITGACDKDSQCGGGCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                 angiogenesis inhibitor; cytostatic; antiinflammatory; cancer; ovarian disease; diabetic retinopathy; inflammatory; ZAQ; Bv8; ISE;
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                        Length 107;
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Pred. No. 2.1e-39;
; Mismatches 0; Indels
                                                     Indels
                        Score 445; DB 7; L
Pred. No. 2.1e-39;
4; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; SEQ ID NO 55; 308pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                      Murine Bv8-related protein - SEQ ID 55.
                                                                                                                                                                                                                                                           ADD69077 standard; protein; 107 AA.
                                                                                                                                                               87 CLPGLACLRTSFNRFICLARK 107
                                                                                                                                                 61 CLPGLACIRTSFNRFICLAOK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Takatsu Y;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            03-FEB-2003; 2003WO-JP001057
                        96.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       04-FEB-2002; 2002JP-00027299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TAKE ) TAKEDA CHEM IND LTD.
                                                                                                                                                                                                                                                                                                                       15-JAN-2004 (first entry)
                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ohtaki T, Masuda Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2003-646310/61.
N-PSDB; ADD69078.
                                        Best Local Similarity
Matches 77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003066860-A1.
Sequence 107 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                   murine; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14-AUG-2003
                                                                                                                                                                                                                                                                                            ADD69077;
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                           Query Match
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                                                      Matches
                                                                                                                                                                                                                              RESULT 37
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The present invention relates to a method (M1) for treating a disorder associated with abnormal haematopoiesis or an autoimmune disorder in a mammal. The method comprises administering antegonists for Bv8 or Endocrine Gland derived Vascular Endothelial Growth Factor (EG-vEGF) to Endocrine Gland derived Vascular Endothelial Growth Factor (KG-vEGF) to the mammal. Bv8 and EG-VEGF are homologues of Vascular Endothelial Growth Factor (VEGF), an angiogenic factor known to have an important role in tumour growth and survival. (M1) is useful for treating abnormal continuous growth and survival. (M1) is useful for treating annormal continuous growth and survival. (M1) is useful for treating immunodeficiency is acute myelotid leukaemia, chronic myelogenous leukaemia, or acute continuous associated with mannodeficiency disorder. Thymphocyte disorder, or lymphodysplastic leukaemia, chronic myelogenous leukaemia, or acute disorder, a primary immunodeficiency disorder, blymphocyte disorder, gecondary immunodeficiency disorder, or a condition associated with an infections disease (H1V infection). The immunodeficiency disorder is a condition associated with an infectious disease (For treating neutropenia, which is associated with an infectious disease (Contental infection). (M1) is useful for treating lymphopaenia or autoimmune disorder such as inflammatory bowel disease, Crohn's disease,
                                                                                                                                                                                                                                                                                                     Antinflammatory; Gastrointestinal; Neuroprotective; Muscular; Antinflammatory; Gastrointestinal; Neuroprotective; Muscular; Antidabetic; Antianemic; haematic; Antithyroid; Hepatotropic; Vitucide; Antidabetic; Antianemic; haematopoiesis; autoimmune disorder; By; Endocrine Gland derived Vascular Endothelial Growth Factor; Ed-VEGF; hematological disorder; leukaemia; myeloproliferative disorder; BG-VEGF; lymphoproliferative disorder; Iymphodysplastic disorder; lymphoproliferative disorder; hiv infection; neutropenia; bacterial infection; lymphopaenia; autoimmune disorder; inflammatory bowel disease; collits; lupus; multiple sclerosis; myasthenia gravis; optic neutritis; psoriasis; rheumatori arthritis; Graves Disease; autoimmune hepatitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Treating disorder associated with abnormal hematopoiesis or autoimmune disorder by administering antagonist of small protein obtained from Bombina variegata or endocrine gland derived vascular endothelial growth
                                                                                                                                                                                                                                                                                Cytostatic; Antimicrobial; Anti-HIV; Immunostimulant; Antibacterial;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 53; SEQ ID NO 6; 161pp; English
                                                                                                            ADS00462 standard; protein; 107 AA
87 CLPGLACLRTSFNRFICLARK 107
                                                                                                                                                                                                                                                 Murine Bv8 homologue, SEQ ID 6.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-MAR-2003; 2003US-0454462P.
14-OCT-2003; 2003US-0511390P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12-MAR-2004; 2004WO-US007622
                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ferrara N, Lecouter J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (GETH ) GENENTECH INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2004-690608/67.
N-PSDB; ADS00461.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         factor, to mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2004081229-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mus musculus.
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Gaps

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1 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP 27 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTFWGQVGDSCHPLTRKVPFWGRRMHHTCP

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Local Similarry, nes 77; Conservative

Matches

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CLPGLACLRISFNRFICLAQK 81

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Gaps

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Indels

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Mismatches

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81; Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying a compound that modulates neurogenesis comprises contacting a neural stem or progenitor cell with a compound that modulates prokineticin receptor signaling and determining its ability to modulate neurogenesis.
             psoriasis, rheumatoid arthritis, Graves Disease, autoimmune hepatitis, type I diabetes or aplastic anaemia. The present sequence is a murine Bv8 sequence used to illustrate the method of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          neurogenesis; prokineticin receptor; PKR; neural stem; progenitor cell; neural regeneration; Alzheimer's disease; Parkinson's disease; neurodegenerative disease; prokineticin 2; PK2.
 lupus, multiple sclerosis, myasthenia gravis, optic neuritis,
                                                                                                                                                                                                    1 AVITGACDKDSQCGCGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFGRRMHHTCP
                                                                                                                                                                                                                         27 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPWGQVGDSCHPLTRKVPFWGRRMHHTCP
                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Amino acid sequence of human prokineticin 2 (PK2) isoform 1.
                                                                                                                             Length 107;
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                                                                                                                              Score 445; DB 8; Le
Pred. No. 2.1e-39;
4; Mismatches 0;
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                                                                                                                                                                                                                                                                                                        CLPGLACLRISFNRFICLARK 107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     04-OCT-2002; 2002US-0416202P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-OCT-2003; 2003WO-US031626,
                                                                                                                              96.5%;
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                                                                                                                                              Local Similarity 95.1
nes 77; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2004-340794/31.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 102 AA;
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Length 102;

Score 440.5; DB 8; Pred. No. 6e-39;

95.68;

Query Match Best Local Similarity

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The invention relates to novel prokineticin-like polypeptides and polynucleotides. The polynucleotide and bolypeptide are useful in diagnostics, forensics, gene mapping, drug screening, identification of mutations responsible for genetic disorders or traits, to assess biodiversity, and to produce many other types of data and products dependent on DNA and amino acid sequences. The polynucleotide and polypeptide may also be used for treating diseases due to impaired gastrophressinal motility (e.g. chronic constipation, diabetic gastrophaesis irritable bowel syndrome or postoperational ileus), for requilating angiogenesis and neovascularization, as well as growth and cavelopment in heart and other tissues, for treating sperm disorders including azoospermia, neurodegenerative diseases (e.g. Alzheimer's disease or Parkinson's disease), autoimmune disorders (e.g. rheumatoid arthritis, diabetes, allergy or astham), wounds, cancer or infections. This sequence corresponds to a protein which has similarity to the novel prokineticin-like proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                    laxative; antiinflammatory; neuroprotective; nootropic; antiparkinsonian; antirheumatic; antiarthritic; antidiabetic; antiallergic; antiasthmatic; vulnerary; cytostatic; antibacterial; virucide; gene therapy; prokineticin; diagnostics; forensics; gene mapping; drug screening; biodiversity; impaired gastrointestinal motility; chronic constipation; diabetic gastroparesis; irritable bowel syndrome; postoperational ileus; angiogenesis; neovascularization; heart; sperm disorder; azoospermia; neurodegenerative disease; Albieimer's disease; Parkinson's disease; autoimmune disorder; rheumatoid arthritis; diabetes; allergy; asthma;
  47
                                       1 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKNNFGNGRQERRKR 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New prokineticin-like polynucleotide and polypeptide for diagnosing, preventing or treating impaired gastrointestinal motility, cancer or neurodegenerative or autoimmune disorders, and for gene mapping or drug
1 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRK-
                                                                                                            KRSKRKKEVPFFGRRMHTCPCLPGLACLRTSFNRFICLAQK 102
                                                                                   ------VPFFGRRMHHTCPCLPGLACLRTSFNRFICLAQK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; SEQ ID NO 14; 132pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drmanac RT;
                                                                                                                                                                                                                                     ADJ71808 standard; protein; 124
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         04-NOV-2002; 2002WO-US035465.
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                                                                                                                                                                                                                                                                                                                      06-MAY-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ghosh MJ, Tang TY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2003-441552/41.
                                                                                                                                                                                                                                                                                                                                                                   Human Bv8 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (HYSE-) HYSEQ INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      wounds; cancer.
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Query Match 95.6%; Score 440.5; DB 7; Length 124; Best Local Similarity 79.4%; Pred. No. 7.2e-39; Matches 81; Conservative 0; Mismatches 0; Indels 21; Gaps
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3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-00-712-355-5
US-10-212-355-5
US-00-513-999-4698
US-09-513-999-4698
US-09-513-999-4698
US-09-161-241-14
US-09-161-241-11
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US-09-161-241-13
US-09-905-125A-236
US-09-905-125A-236
US-09-905-1238-236
US-09-905-138-236
US-09-905-318-236
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Maximum Match 100%
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sednence sed		100.0%; Score 461; DB 4; Length 108; conservative 0; Mismatches 0; Indels 0; Gaps AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRWHHTCP AVITGACDKDSQCGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRWHHTCP AVITGACDKDSQCGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRWHHTCP CLPGLACLRTSFNRFICLAQK 81 [CLPGLACLRTSFNRFICLAQK 108	
		44; Length 10 44; 0; Indels LGDSCHPLTRKVP LGDSCHPLTRKVP	
9-949-016-7859 9-161-241-8 9-161-241-8 9-188-930-192 9-312-283C-192 9-312-283C-192 9-489-845-83A-10 9-561-709B-3 9-188-432-16 8-93-232-16 8-93-232-19 9-121-457-1 9-561-818A-24	ENTS : 5	61; DB 7.1e- trches RICTPMGK	8 201A 9
US-09-949-00-949-00-9-049-00-9-49-00-9-049-00-9-04-00-9-0-18-09-18-0-9-18-0-9-9-18-0-9-9-9-9-9-9-9-9-9-9-9-9-9-9-9-9-9-9-	ALIGNMENTS 9712529 O. Ore E. Zven Proteins US/09/712,529 -11-14 lows Version 3.0	Score 461; Pred. No. 7. 0; Mismatches AVSIWVKSIRICTP	in 2, 52
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200.00 110.00 10	ALIGA OB-712-529-2 equence 2, Application US/09712529 atent No. 648538 ENERAL INFORMATION: APPLICANT: Sheppard, Paul O. APPLICANT: Whitmore, Theodore E. APPLICANT: Thompson, Paul D. APPLICANT: Thompson, Paul D. APPLICANT: Thompson, Paul D. APPLICANT: Thompson, Paul D. APPLICANT: Histore, Theodore E. APPLICANT: Thompson, Paul D. TITLE OF INVENTION Human Zwen Frote FILE REFERENCE: 99-81 TURENT APPLICATION NUMBER: US/09/712 CURRENT FILING DATE: 2000-11-14 NUMBER OF SEQ ID NOS: 7 LENGYTH: 108 TYPE: FastSEQ for Windows Versio EQ ID NO 2 LENGYTH: 108 TYPE: PRT ORGANISM: Homo sapiens	Similarity 100.0%; Similarity 100.0%; In Conservative 0; AVITGACDKDSQCGGGMCGAVGAVITGACDKDSQCGGGMCCAVGAVITGACDKDSQCGGGMCCAVGAVITGACLRTSFNRFICLAQK	RESULT 2 US-10-212-201A-2 Sequence 2, Application US/10212201A FERENT NO. 675649 GENERAL INFORMATION: APPLICANT: Sheppard, Paul O. APPLICANT: Bishop, Paul D. APPLICANT: Whitmore, Theodore E. APPLICANT: Thompson, Penny P. TITLE OF INVENTION: Human Zven Prote FILE REFERENCE: 99-81 CURRENT FILING DATE: 2002-08-02 PRIOR APPLICATION NUMBER: US/10/21 CURRENT FILING DATE: 2002-08-02 PRIOR APPLICATION NUMBER: US/09/712, NUMBER OF SEQ ID NOS: 7
98 90.55 73.55 73.55 73.55 73.57 71.57 71.57 71.55 71.	ESULT 1 S-09-712-529-2 Sequence 2, Applicate to 648593 GENERAL INFORMATICANT: Shepl APPLICANT: Shepl APPLICANT: Shepl APPLICANT: Which APPLICANT: Which APPLICANT: Which APPLICANT: Thomp TITLE OF INVENTIFIED FILE REFRENCE: CURRENT FILING D NUMBER OF SEQ ID NO 2 LENGTH: 108 LENGTH: 1	Query Match Best Local Sin Matches 81; / 1 A c 28 A y 61 C	12-201A. 12-201A. 12-201A. 12-201A. 12-201A. 11-201CANT: 11-201CANT: 11-20NT: 11-20N
8 0 0 0 11 12 14 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4	RESULT 1 US-09-712-529 Sequence 2, Patent No.; GENERAL ING. APPLICANT: APPLIC	Query Best I Matche Qy Db Oy Oy	RESULT 2 US-10-212. Sequence Pacent Pacent APPLIC A

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20 AVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKRKHHTCP 79
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                                                  63.1%; Score 291; DB 4; Length 105; 58.4%; Pred. No. 4.8e-25; Live 14; Mismatches 18; Indels
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APPLICANT: Sheppard, Paul O.
APPLICANT: Bishop, Paul O.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Whitmore, Penny P.
TITLE OF INVENTION: Human Zven Proteins
FILE REFERENCE: 99-81
CURRENT APPLICATION NUMBER: US/10/212,201A
CURRENT FILING DATE: 2002-08-02
PRIOR FILING DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Shappard, Paul O.
APPLICANT: Bishop, Paul D.
APPLICANT: Whitmore, Theodore E.
APPLICANT: Thompson, Penny P.
TITLE OF INVENTION: Human Zven Proteins
FILE REFERENCE: 99-81
CURRENT APPLICATION NUMBER: US/10/212,355
CURRENT APPLICATION NUMBER: 2002-08-02
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
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; Patent No. 6756479
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; Patent No. 6828425
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                                               Query Match
Best Local Similarity 58.4%
Matches 45; Conservative
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Best Local Similarity 58.4%
Matches 45; Conservative
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; LENGTH: 105
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-212-355-5
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LENGTH: 105
US-09-712-529-5
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100.0%; Score 461; DB 4; Length 108;
Best Local Similarity 100.0%; Pred. No. 7.1e-44;
Matches 81; Conservative 0; Mismatches 0; Indels
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PATENT NO. 648538
GENERAL INFORMATION:
APPLICANT: Sheppard, Paul O.
APPLICANT: Bishop, Paul D.
APPLICANT: Thompson, Penny P.
TITLE OF INVENITON: Human Zven Proteins
FILE REFERENCE: 99-81
CURRENT FILLION UNMERR: US/09/712,529
CURRENT FILLION DATE: 2000-11-14
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Whitmore, Theodore E.
APPLICANT: Thompson, Penny P.
TITLE OF INVENTION: Human Zven Proteins
FILE REFERENCE: 99-81
CURRENT APPLICATION NUMBER: US/10/212,355
CURRENT FILING DATE: 2002-08-02
NUMBER OF SEQ ID NOS: 7
SOFTWARE: FastSEQ for Windows Version 3.0
  SOFTWARE: FastSEQ for Windows Version 3.0
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APPLICANT: Sheppard, Paul O.
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LENGTH: 105
TYPE: PRT
ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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US-10-212-201A-2
                         SEQ ID NO 2
LENGTH: 108
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LENGTH: 108
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US-10-212-355-2
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Sequence 4698, Application US/09513999C

Sequence 4698, Application US/09513999C

Patent No. 6783961

APPLICANT: Dumas Milne Edwards, J.B.

APPLICANT: Duclert, A.

APPLICANT: Duclert, A.

TITLE OF INVENTION: Expressed Sequence Tags and Encoded Human Proteins.

Patent No. 6783961

FILE REPERENCE: 59.US2.REG

CURRENT APPLICATION NUMBER: US/09/513,999C

CURRENT FILING DATE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTHARE: PROFESSED SEGUENCE: 1999-02-26

NUMBER OF SEQ ID NOS: 36681

SOFTHARE: PROFESSED SEGUENCE: DATE: US SOFTHARE: US 
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61.6%; Score 284; DB 4; Length 105;
Best Local Similarity 55.8%; Pred. No. 2.8e-24;
Matches 43; Conservative 15; Mismatches 19; Indels
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; Sequence 5350, Application US/09621976
; Patent No. 663963
; GENERAL INFORMATION:
; APPLICANT: Dumas Milne Edwards, J.B.
; APPLICANT: Glordano, J.Y.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; TITLE OF INVENTION: ESTS and Encoded Human Proteins.
; CURRENT APPLICATION NUMBER: US/09/621,976
; CURRENT APPLICATION NUMBER: 2000-07-21
; NUMBER OF SEQ ID NOS: 19335
; SOFTWARE: Patent.pm
; SEQ ID NO 5350
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; OTHER INFORMATION: Xaa = Ala,Gly
US-09-621-976-5350
Tue Nov 8 09:17:14 2005
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Matches 45; Conservative
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ORGANISM: Homo sapiens
FEATURE:
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NAME/KEY: UNSURE
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US-09-621-976-5350
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LENGTH: 80
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144 SCLRTFDCGPGLCCARHFWIK---ICKPVLLEGQVCSRRGHKDTAQAPEIFQR----CDC 196
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                                                                                                                                 55.5%; Score 256; DB 4; Length 80; 60.7%; Pred. No. 2.7e-21; ive 14; Mismatches 10; Indels
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Sequence 10, Application US/09161241

SEQUENCE No. 6344541

GENERAL INFORMATION:

APPLICANT: Bass, Michael B

APPLICANT: Theill, Lars E

APPLICANT: Theill, Lars E

APPLICANT: Theill, Lars E

APPLICANT: Mang, Daguang

TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES

FILE REFERENCE: A-548

CURRENT APPLICATION NUMBER: US/09/161,241

CURRENT FILING DATE: 1998-09-25

NUMBER OF SEQ ID NOS: 78
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Bass, Michael B
APPLICANT: Bass, Michael B
APPLICANT: Sullivan, John K
APPLICANT: Theill, Lars E
APPLICANT: Wang, Daguang
TITLE COF INVENTION: NOVEL DKR POLYPEPTIDES
FILE REFERENCE: A-548
CURRENT APPLICATION NUMBER: US/09/161,241
CURRENT FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 78
SOFTWARE: Patentin Ver. 2.0
                     LOCATION: -19...1
COTHER INFORMATION: SCORE 7.2
CHER INFORMATION: SEQ VSIMILLIVIVSDC/AV
US-09-513-999C-4698
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; Sequence 14, Application US/09161241
; Patent No. 6344541
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                                                                                                                                        Query Match
Best Local Similarity 60.7%
Matches 37; Conservative
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ORGANISM: Human
NAME/KEY: SIGNAL
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ORGANISM: Human
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US-09-161-241-10
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LENGTH: 224
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                                                                              9
                                                                                                    20 AVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKKKHHTCP 79
                                                                           1 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP
                               Gaps
                               .
       58.4%; Pred. No. 4.8e-25;
tive 14; Mismatches 18; Indels
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Gaps

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FILE REFERENCE: CLOOL307.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
TILE REFERENCE: CLOOL307
TILE REFERENCE: CLOOL307
FILE REFERENCE: CLOOL
                                                                                                                                                 183 CLRSSDCIDGFCCARHFWTK---ICKPVLHQGEVC-TKORKKGSHGLEIFORCDCAKGLS 238
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                                                                                          7 CDXDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCPCLPGLA
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                                Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 97; DB 3; Length 207; Pred. No. 0.003;
                             Indels
Best Local Similarity 36.1%; Pred. No. 0.0029;
Matches 22; Conservative 5; Mismatches 30;
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APPLICANT: Bass, Michael B
APPLICANT: Sullivan, John K
APPLICANT: Theill, Lars E
APPLICANT: Wang, Daguang
TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
FILE REFERENCE: A-54
CURRENT APPLICATION NUMBER: US/09/161,241
CURRENT FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 13
LENGTH: 207
                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 7146, Application US/09949016 Patent No. 6812339
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21.0%;
36.1%;
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Matches 22; Conserva
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Best Local Similarity
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US-09-949-016-7146
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US-09-161-241-13
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US-09-161-241-13
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US-09-976-584-1086
US-09-976-584-1086
Sequence 1086, Application US/09976594
Patent No. 6673349
GENERAL INFORMATION:
APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
TITLE OF INVENTION UNDER: US/09/976,594
CURRENT APPLICATION NUMBER: US/09/976,594
FRIOR PILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOFTWARE: PERL PROGRAM
SEQ ID NO 1086
LENGTH: 266
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                                                                                                                                                        7 CDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCPCLPGLA
                                                                                                 4; Gaps
                             Query Match 21.7%; Score 100; DB 3; Length 266; Best Local Similarity 37.7%; Pred. No. 0.0018; Matches 23; Conservative 5; Mismatches 29; Indels
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US-09-976-594-1086
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APPLICANT: Bass, Michael B
APPLICANT: SUllivan, John K
APPLICANT: Theill, Lars E
APPLICANT: Wang, Daguang
TITLE OF INVENTION: NOVEL DKR POLYPEPTIDES
FILE REFERENCE: A-548
CURRENT APPLICATION NUMBER: US/09/161,241
CURRENT FILING DATE: 1998-09-25
NUMBER OF SEQ ID NOS: 78
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 11
LENGTH: 259
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Patent No. 6344541
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ORGANISM: Homo sapiens
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ORGANISM: Mouse
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US-09-161-241-11
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309.179 Million cell updates/sec
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| cgn2_6/ptodata/1/pubpaa/USO7_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/USO7_NEW_PUB.pep:*
7: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
8: /cgn2_6/ptodata/1/pubpaa/USO8_NEW_PUB.pep:*
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GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.
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US-10-417-45-5
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US-10-467-019-19
US-10-467-019-19
US-10-713-567-6
US-10-811-328-6
US-10-912-724-6
US-10-977-113-9
US-10-977-113-9
US-10-871-152-18
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                                                                                                                                                                                                                                                                                                                                                                    1867879 seqs, 418409474 residues
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Maximum Match 100%
Listing first 45 summaries
                                                                                     OM protein - protein search, using sw model
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Maximum DB seq length: 2000000000
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461
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<u> </u>	Sequence 19, Appl. Sequence 71, Appl. Sequence 9, Appl. Sequence 29, Appl. Sequence 29, Appl. Sequence 31, Appl. Sequence 31, Appl.
00-503-954A	US-10-467-019-39 US-10-680-554-71 US-10-680-554-11 US-10-713-567-29 US-10-713-567-29 US-10-713-567-31 US-10-811-328-31
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1132 11432 1165 1174 1174 1174 1174 1174 1174 1174 117	3

ALIGNMENTS

1 AVITGACDKDSQCGGGGCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP Gaps ; 0 100.0%; Score 461; DB 13; Length 81; 100.0%; Pred. No. 9.6e-44; ive 0; Mismatches 0; Indels (APPLICANT: Enlert, Frederick
TITLE OF INVENTION: Prokineticin Polypeptides, Related
TITLE OF INVENTION: Compositions and Methods
TITLE OF INVENTION: Compositions and Methods
FILE REFERENCE: P-UC 5016
CURRENT APPLICATION NUMBER: US/10/016,481
CURRENT FILING DATE: 2001-11-01
PRIOR APPLICATION NUMBER: 60/245,882
PRIOR FILING DATE: 2000-11-03
SOPTHARE: FASTESEQ for Windows Version 4.0
SEQ ID NO 6; ; Sequence 6, Application US/10016481; Publication No. US20020115610A1; GENERAL INFORMATION: 81; Conservative TYPE: PRT ORGANISM: Homo sapiens Query Match Best Local Similarity US-10-016-481-6 US-10-016-481-6 Matches

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61 CLPGLACLRISFNRFICLAOK 81 CLPGLACLRTSFNRFICLAQK 81

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RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 100.0%; Score 461; DB 14; Length 81; Best Local Similarity 100.0%; Pred. No. 9.6e-44; Matches 81; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 100.0%; Score 461; DB 15; Length 81; Best Local Similarity 100.0%; Pred. No. 9.6e-44; Matches 81; Conservative 0; Mismatches 0; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Squence 5, Application US/10417426

Dublication No. US2003023535A1

GENERAL INFORMATION:
APPLICANT: Zhou, Qun-Yong
APPLICANT: Bullock, Clayton M.
TITLE OF INVENTION: Screening and Therapeutic Methods For TITLE OF INVENTION: Treating Circadian Rhythm Disorders; FILE REFERENCE: P-UC 5773
CURRENT FILING DATE: 2003-04-15
PRIOR PILING DATE: 2003-04-15
PRIOR PILING DATE: 2002-04-15
NUMBER OF SEQ ID NOS: 21
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 81
                                Sequence 6, Application US/10323157

Publication No. US20030113867A1

GENERAL INFORMATION:
APPLICANT: Zhou, Qun-Yong
APPLICANT: Ehlert, Frederick
TITLE OF INVENTION: Prokineticin Polypeptides, Related
TITLE OF INVENTION: Prokineticin Rehods
FILE REFERENCE: P-UC 5016
CURRENT FPLING DATE: 2002-12-18
PRIOR FILING DATE: 2001-11-01
PRIOR FILING DATE: 2001-11-01
PRIOR FILING DATE: 2001-11-03
NUMBER OF SEQ ID NOS: 19
SOFTWARE: PateSEQ for Windows Version 4.0
SEQ ID NO 6
LENGTH: 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 CLPGLACLRTSFNRFICLAQK 81
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                                                                                                                                                                                                                                                                                                                                                                                                                                   ; ORGANISM: Homo sapiens
US-10-323-157-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
RESULT 2
US-10-323-157-6
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US-10-467-019-19
Sequence 19, Application US/10467019
Sequence 19, Application US/10467019
Sequence 19, No. US20040048314A1
GENERAL INFORMATION:
APPLICANT: Takeda Chemical Industries, Ltd.
TITLE OF INVENTION:
CURRENT APPLICANT: P01-0295 PCT
CURRENT APPLICATION NUMBER: US/10/467,019
CURRENT FILING DATE: 2003-08-01
PRIOR APPLICATION NUMBER: J22001-026820
SPRIOR FILING DATE: 2001-02-02
NUMBER OF SEQ ID NOS: 71
SEQ ID NO 19 9 1 AVITGACDKDSQCGGGGCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHTCP 60 9 1 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHTCP 60 1 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP 1 AVITGACDKDSQCGCGCGCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP Gaps ö .; 0 Length 81; Length 81; Indels Indels Sequence 7, Application US/10680554

Publication No. US20040229291A1

GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: Cheng, Michelle Y.

TITLE OF INVENTION: Screening and Therapeutic Methods:

TITLE OF INVENTION: Relating to Neurogenesis

FILE REFRENCE: 66778-356

CURRENT FILING DATE: 2003-10-03

PRIOR APPLICATION NUMBER: US 60/416,202

PRIOR APPLICATION NUMBER: US 60/416,202

PRIOR APPLICATION NUMBER: 202-10-04

NUMBER OF SEQ ID NOS: 21

SOFTWARE: FRSENCE for Windows Version 4.0 ch 100.0%; Score 461; DB 15; 1 Similarity 100.0%; Pred. No. 9.6e-44; 81; Conservative 0; Mismatches 0; ; Score 461; DB 16; ; Pred. No. 9.6e-44; 0; Mismatches 0; 61 CLPGLACLRISFNRFICLAQK 81 61 CLPGLACLRISFNRFICLAOK 81 US-10-713-567-6

Sequence 6, Application US/10713567

Publication No. US2040235732A1

GENERAL INFORMATION:
APPLICANT: Zhou, Qun-Yong 100.0%; 81; Conservative ; ORGANISM: Homo sapiens US-10-680-554-7 Query Match Best Local Similarity Matches 81; Conserv Query Match Best Local Similarity Matches 81; Conserv TYPE: PRT ORGANISM: Human US-10-467-019-19 US-10-680-554-7 LENGTH: 81 SEQ ID NO 7 TYPE: PRT

GenCore version 5.1.6 Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

November 7, 2005, 20:48:31; Search time 23:2814 Seconds (without alignments)
334.754 Million cell updates/sec Run on:

US-10-811-328-6 461 Title: Perfect score:

1 AVITGACDKDSQCGGGMCCA.....LPGLACLRISFNRFICLAQK 81 BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table: Sequence:

283416 seqs, 96216763 residues Searched:

283416 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

PIR_79:*
1: pirl:*
2: pir2:*
3: pir3:*
4: pir4:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Description	REIC protein - hum	MEGF6 protein - ra	laminin alpha-1 ch	hypothetical prote	cell-fate determin	laminin gamma-1 ch	gastric mucin MUCS	jagged protein pre	cytochrome-c3 hydr	EGF repeat transme	cytochrome-c3 hydr	laminin alpha-1 ch	colipase precursor	hypothetical prote		hypothetical prote	colipase precursor	tenascin-X - bovin	notch 3 protein -	keratin high-sulfu	keratin-like prote	protein F11C7.4 [i	agrin precursor -	notch3 protein - h	hypothetical prote	high cysteine chor	cell wall glycopro	9.	hypothetical prote
COLUMN TO COLUMN	ID	JC7188	T13954	S18253	T16271	A49128	MMHUB2	S56015	A56136	S08198	T30176	HQDVSG	S14458	151909	T16210	T27283	T34264	XTHO	T42629	S45306	KRSHA3	I38025	E89753	AGCH	S78549	T22812	B21761	S50062		T32497
	DB	2		~		•																	•		~					
	Query Match Length	350	1574	3712	264	2471	1609	850	1220	313	1687	314	3075	112	1599	1620	2195	112	4135	2318	131	257	1722	1955	2321	3871	143	442	1522	2150
de	Query Match	20.6	16.6	16.5	16.1	15.9	15.3	15.2	14.9	•	14.6	14.5	14.4	14.3	14.2	14.2	14.2	14.1	14.1	14.0	13.9	13.9	13.9	13.9	13.8	13.8	13.7	13.7	13.7	13.7
	Score	95	76.5	16	74	73.5	70.5	70	68.5	89	67.5	67	66.5	99	65.5	65.5	65.5	65	65	64.5	64			64	63.5	63.5	63	63	63	63
	Result No.	-	8	m	4	'n	9	7	80	σ	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24		26	27	28	29

tenascin-X precurs mucin, submaxillar	probable membrane aqrin - rat	laminin alpha 5 ch	high-cysteine chor	CD27 antigen precu	hypothetical profe	fertilin alpha-11	fertilin alpha-I	protein CTRP - mal	hypothetical prote	protein T22H2.6 [1	hypothetical prote	hypothetical prote	epithelin/granulin
A40701 T03099	S67091 AGRT	T10053	A23219	A49053	H69609	855060	855059	T18397	H75434	E87929	T25138	T25137	B38128
7 7	~ -	1 (1	~	႕	~	~	~	~	N	~	N	~	0
3566	109	3635	178	250	297	825	905	2098	203	318	345	358	589
13.7	13.6	13.6	13.4	13.4	13.4	13.4	13.4	13.4	13.3	13.3	13.3	13.3	13.3
63 63	62.5	62.5	62	62	62	62	62	62	61.5	61.5	61.5	61.5	61.5
30 31	32	. w	35	36	37	38	6	40	41	42	4.3	44	45

ALIGNMENTS

	RESULT 1 JC7188 REIC protein - human C.Sneries: Homo sariens (man)
	C;Date: 04-Mar-2000 #sequence_revision 04-Mar-2000 #text_change 11-May-2000 C;Accession: UCT188 R:Pangi T: Mivazaki M.; Sakaquchi, M.; Inoue, Y.; Namba, M.
	Biochem. Biophys. Res. Commun. 268, 20-24, 2000 A;Title: A REIC gene shows down-regulation in human immortalized cells and human tumor-A;Reference number: JC7188; MUID:20119095; PMID:10652205
	A;Accesion: JC7188 A;Aclecule type: mRNA A;Residues: 1-350 <tsu></tsu>
	A;Cross-references: DDBJ:AB034203 A;Experimental source: heart C;Comment: This protein is a secreted glycoprotein for head induction in amphibian embr
	C;Genetics: A.A.gene: real: C;Superfamily: human REIC protein C;Keywords: cardiac muscle; coiled coil; glycoprotein; heart; tumor
_	O Metch 20 6%. Score 95: DB 2: Length 350;

4 7 CDKDSQCGGGCGAVSIWVKSIRICTPMGKLGDSCH-PLTRKVPFFGRRMH-----HTCP 60 8 20.6%; Score 95; DB 2; Lengtn 350 29.5%; Pred. No. 0.0072; tive 11; Mismatches 36; Indels Query Match Best Local Similarity 29.5 Matches 23; Conservative ઠે

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267 CASGLLCQPHSHSPVYVC 284 61 CLPGLACLRISFNR-FIC 77 g ò

T13954 MEGF6 p

protein - rat

C;Species Rattus norvegicus (Norway rat)
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T13954
R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
R;Nakayama, M.; Nakajima, D.; Nagase, T.; Nomura, N.; Seki, N.; Ohara, O.
A;Reference number: Z14126; MUID:9836089; PMID:9693030
A;Residues: I-1574 <NAK>
A;Residues: I-1574 <NAK>
A;Residues: I-1574 <NAK>
A;Cross-references: UNIPROT:088281; EMBL:AB011532; NID:93449293; PIDN:BAA32462.1; PID:976908.
A;Experimental source: strain Sprague-Dawley; brain
C;Genetics:
A;Gene: MEGF6

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A;Residues: 1-264 <CON>
A;Cross-references: UNIPROT:020043; EMBL:U28741; NID:g861290; PID:g861291; PIDN:AAA6832!
A;Experimental source: strain Bristol N2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         37 SIVNGKCECTLRYEGPQCERERCLNGGRRHSAKG----TVRCHCPYGLSGDRCEKVTYCE 92
                                                                                                                                                                                                                                          hypothetical protein F35D2.3 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Accession: T16271 R;Connell, M. R;Connell, M. A;Description: The sequence of C: elegans cosmid F35D2. A;Description: The sequence of C: elegans cosmid F35D2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-Jan-1994 #sequence_revision 18-Nov-1994 #text_change 16-Aug-2004
C;Accession: A49128
A;Title: Notch: W.J.; Lemke, G.
A;Title: Notch: a second mammalian Notch gene.
A;Reference number: A49128; MUID:93202015; PMID:1295745
A;Accession: A49128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               7 CDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCPCLPGLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A.Status: preliminary, not compared with conceptual translation A.Molecule type: mRNA A.Molecule type: mRNA A.Molecule type: mRNA A.Molecule type: mRNA A.Rosacidus: 1-2471 - WMEI. A.Cross-references: UNIPROT: 090W30 A.Experimental source: Schwann cell A.Note: sequence extracted from NCBI backbone (NCBIP:127811) G.Superfamily: Notch protein; ankyrin repeat homology; EGF homology F;264-295/Domain: EGF homology eEGF1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    7;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                33; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;1909-1941/Domain: ankyrin repeat homology <AN2>F;1943-1975/Domain: ankyrin repeat homology <AN3>F;1943-1008/Domain: ankyrin repeat homology <AN3>F;19709-2041/Domain: ankyrin repeat homology <AN4>F;2009-2041/Domain: ankyrin repeat homology <AN4>F;2009-2041/Domain: ankyrin repeat homology <AN5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 16.1%; Score 74; DB 3
Best Local Similarity 28.1%; Pred. No. 1;
Matches 25; Conservative 11; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PFFGRRMHHTCPCL --- PGLAC-LRTSFN 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          F;1876-1908/Domain: ankyrin repeat homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;1029-1060/Domain: EGF homology <EGF>
F;1067-1098/Domain: EGF homology <EGX3>
F;1153-1184/Domain: EGF homology <EGF3>
F;1191-1222/Domain: EGF homology <EGF3>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EGF homology < EGX2 >
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Genetics:
A;Gene: CESP:F35D2.3
A;Introns: 40/3; 71/3; 160/3; 197/3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15.9%;
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Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Accession: T16271
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   49
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Fig. 776-2115/Domain: laminin-type EdF-like homology tiesus;
Fig. 776-2115/Domain: laminin-type EGF-like homology tiesus;
Fig. 1909-1856/Domain: laminin-type EGF-like homology tiesus;
Fig. 1917-1957/Domain: laminin-type EGF-like homology tiesus;
Fig. 1917-1957/Domain: laminin-type EGF-like homology tiesus;
Fig. 1917-2061/Domain: laminin-type EGF-like homology tiesus;
Fig. 1917-2061/Domain: laminin-type EGF-like homology tiesus;
Fig. 1917-2061/Domain: laminin-type EGF-like homology tiesus;
Fig. 1918-2061/Domain: repeat GI kRG1>
Fig. 1918-2061/Domain: repeat GI kRG1>
Fig. 1918-2061/Domain: repeat GI kRG2>
Fig. 1918-2061/Domain: repeat GI kRG3>
Fig. 1
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A;Retues baselor acid
A;Residues 1.312 (2003)
A;Cross-references: UNIPROT:(000174; GB:M9638B; NID:g157799; PIDN:AAA28662.1; PID:g157800
B;Garrison, K.; MacKrell, A.J.; Pessler, J.H.
J. Biol. Chem. 266, 22809-22904, 1991
A;Title: Drosophila laminin A chain sequence, interspecies comparison, and domain struct
A;Reference number: S18253; MUID:92078147; PMID:1744083
A;Molecule type: mRNA
A;Residues: 1762-3712 (GAR>
A;Molecule type: mRNA
A;Residues: 1762-3712 (GAR>
A;Cross-references: EMBL:M75882; NID:g157797; PIDN:AAA28661.1; PID:g157798
C;Genetics:
C;Genetics:
A;Gene FlyBase: LanA
A;Cross-references: FlyBase: FBgn0002526
C;Genetics:
C;Ckeywords: basement membrane; cell binding; coiled coil; disulfide bond; extracellular
C;Keywords: basement membrane; cell binding; coiled coil; disulfide bond; extracellular
F;273-330/Domain: laminin-type EGF-like homology <LEG>
F;373-400/Domain: laminin-type EGF-like homology <LEG>
F;1776-2115/Domain: laminin-type EGF-like <LEG
F;1776-211605/D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    laminin alpha-1 chain precursor - fruit fly (Drosophila melanogaster)
C;Species: Drosophila melanogaster
C;Date: 16-Sep-1992 #sequence_revision 24-Jul-1997 #text_change 09-Jul-2004
C;Accession: 528399; 518253
R;Kusche-Gullberg, M.; Garrison, K.; MacKrell, A.J.; Fessler, L.I.; Fessler, J.H.
EMBO J. 11, 4519-4527, 1992
A;Title: Laminin A chain: expression during Drosophila development and genomic sequence.
A;Reference number: S28399; MUID:93049203; PMID:1425586
                                                                                                                                                                                                                                                                                                                                 960 CDSACNCSAGAPCDA---VTGSCIC-PAGRWGPRCAQSCPPLT-----FGLNCSQICTCF 1010
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                                                                                                                                                                                                                                                     ---DSCHPLTRKVPFFGRRMHTCPCL
                                                                                                                                                         Gaps
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                                                                                                                                               28; Indels 13;
                                                   DB 2; Length 1574;
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16.5%; Score 76; DB 2
Best Local Similarity 30.7%; Pred. No. 5.7;
Matches 27; Conservative 5; Mismatches
                                             Query Match
16.6%; Score 76.5; DE
Best Local Similarity 33.8%; Pred. No. 2.5;
Matches 22; Conservative 2; Mismatches
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GenCore version 5.1.6

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OM protein - protein search, using sw model

Run on:

November 7, 2005, 20:47:46; Search time 110.587 Seconds

(without alignments)
375.076 Million cell updates/sec

Perfect score: 461
Sequence: 1 AVITGACDKDSQCGGGMCCA......LPGLACLRTSFNRFICLAQX 81

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378
```

use: Uniprot_O3:*
1: uniprot_sprot:*
2: uniprot_trembl:*
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution:

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

Minimum DB seq length: 0 ... Maximum DB seq length: 2000000000

SUMMARIES

SUMMALES		Description	Q8r413		Q863h4	09dxn1	Q6v8j7	Q863h5	ENPO	JMAN P58294 homo	Q8tc69	\tag{88r414}	Q8k457	TVA Q9pw66	08j £40	Q8jfe6	Q8jfx9 bombina	Q8j fy1	Q8j fy0	Q8jfx8 l	Q8jfy2	Q8vej3	Q8uux3 gall	OUSE 054908 mus	.5 Q80u15	JMAN Q9ubt3	O9pwh3	UMAN 094907	09dda4	OUSE 094yz8	Q8bfw0	JS Office	
Ď		ΩI	PRK2	PRK2	Q863H	PRK2	Q6V8J7	0863H5	VPRA	PRK1 H	QBTC6	PRK1 R	Q8K45	BV8 B	QBJFQ0	QBJFE6	QBJFX9	QBJFY1	QBJFYO	OBJEX8	QBJFY2	08VEJ3	QBUUX3	DKK1	QBOULS	DKK4	Q9PWH3	DKK1	Q9DDA4	DKK2	OBBEWO	OGPVUS	
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		Match Length	107	129	108	128	128	128	81	105				96	96	96	96	96	96	96	96	221	96	272	272	224	240	266	255	259	259	268	
•	ouery		96.5	95.6	92.4	92.1	92.1	88.1	67.8	63.1	62.9	62.0	55.7	53.9	53.9	50.7	50.4	50.4	49.9	48.9	47.4	24.4	23.9	22.3	22.3	22.0	21.7	21.7	21.5	21.3	21.3	21.3	
		ore	445	440.5	426	424.5	424.5	406	312.5	291	290	286	257	248.5	248.5	233.5	232.5	232.5	230	225.5	218.5	112.5	110	103	103	101.5	100	100	66	86	86	86	
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Ogubp4 homo sapien	Q8n294 homo sapien Q90839 gallus gall	Q9w6d9 brachydanio	Oggans mus musculu	O57464 xenopus lae	Q6pq81 homo sapien	Q9tts4 bos taurus	Q8spm4 bos taurus	Q8mtx1 caerostris	Q8vhf4 mus musculu	Q8cga7 mus musculu
043532 DKK3_HUMAN	Q8N294 DKK3 CHICK	Q9W6 <u>D</u> 9	DKK3 MOUSE	057464	Q6PQ81	Q9TTS4	Q8SPM4	TXCA CAEEX	Q8VHF4	Q8CGA7
7 7	7 7	20	v ~	7	~	~	~	٦	7	7
171 350	215 350	241	349	259	350	564	5146	102	747	1004
20.6	20.5	20.0	19.8	19.5	19.3	17.7	17.7	17.2	17.2	17.2
95 95	94.5	92	90.5	90	89	81.5	81.5	79.5	79.5	79.5
32 33	34 7	36	3.8	0 0 0	4	41	42	43	44	45

ALIGNMENTS

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81; Conservative
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34
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68
109
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TISSUE SPECIFICITY: Expressed in the testis and, at low levels, in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                27 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPWGQVGDSCHPLTRKVPFWGRRMHTCP
                                                                                                                                                                                                                                                                                                                                                       MEDLINE=20047850, PubMed=10580115; DOI=10.1016/S0014-5793(99)01473-8; Wechselberger C., Puglisi R., Lepperdinger G., Boitani C., Kreil G.; "The mammalian homologue of Bv8 from frog skin is mainly expressed in
                                                                                                                                           1 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP
                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                     Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=21160229; PubMed=11259612;
Li M., Bullock C.M., Knauer D.J., Ehlert F.J., Zhou Q.-Y.;
"Identification of two prokinetricin cDNAs: recombinant proteins
potently contract gastrointestinal smooth muscle.";
Mol. Pharmacol. 59:692-698(2001).
                                                                                                                           ö
                                                                                                          Length 107;
                                                                                                            9.2e-42;
0; Indels
                                                                                          BDFF316CDCB5FED0 CRC64;
                                                                                                                                                                                                                                                     16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Prokineticin 2 precursor (PK2) (Protein Bv8 homolog).
Name-PROK2; Synonyms-BV8;
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Event=Alternative splicing; Named isoforms=2;
                                                                                                          Score 445; DB 1;
Pred. No. 9.2e-42;
                                Potential.

Prokineticin 2.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
                                                                                                                                                                                                                                      129 AA.
                                                                                                                           4; Mismatches
InterPro; IPR009523; Prokineticin.
Pfam; PF06607; Prokineticin; 1.
Biological rhythms; Neuropeptide; Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IsoId=Q9HC23-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 5-129 FROM N.A. (ISOFORM 1).
                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                     61 CLPGLACLRTSFNRFICLAQK 81
                                                                                          11594 MW;
                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A. (ISOFORM 2)
                                                                                                                                                                                                                                                                                                                                                                                         FEBS Lett. 462:177-181(1999).
                                                                                                         96.5%;
                                                                                                                          77; Conservative
                                                                                                                                                                                                                                      STANDARD;
                                 26
107
45
57
85
93
103
                                                                44
67
87
107 AA;
                                                                                                           Query Match
Best Local Similarity
Matches 77; Conserv
RGD; 620280; Bv8
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                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GO; GO:000556; C:extracellular; TAS.
GO; GO:000164; F:G-protein-coupled receptor binding; TAS.
GO; GO:000187; P:activation of MAPK; TAS.
GO; GO:0001825; P:anti-apoptosis; IDA.
GO; GO:0006916; P:anti-apoptosis; IDA.
GO; GO:0006915; P:chemotaxis; IDA.
GO; GO:0007204; P:chemotaxis; IDA.
GO; GO:0007204; P:chemotaxis; IDA.
GO; GO:0007204; P:chemotaxis; IDA.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; NAS.
GO; GO:0019233; P:inflammatory response; NAS.
GO; GO:0019233; P:perception of pain; TAS.
GO; GO:0017833; P:spermatogenesis; IMP.
the small intestine. INDUCTION: Activated by CLOCK and BMAL1 heterodimers and light; inhibited by period genes (PER1, PER2 and PER3) and cryptochrome genes (CRY1 and CRY2) (Probable). SIMILARITY: Belongs to the prokinecitin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam, PF06607; Prokineticin, 1.
Alternative splicing; Biological rhythms; Direct protein sequencing;
Neuropeptide; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
01-MR-2004 (TrEMBLrel. 26, Last annotation update)
Bv8/prokineticin 2-like protein splice variant.
Bos taurus (Bovine).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi, Mammalia; Eutheria, Cetartiodactyla; Ruminantia; Bovidae; Bovinae; Bos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -----VPFFGRRMHHTCPCLPGLACLRTSFNRFICLAQK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0487679E8700DA55 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Prokineticin 2.
By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
Missing (in isoform 2).
/FTIG-VSP_005219.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .5e-41;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 440.5; D
Pred. No. 3.5e-
0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     108 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IPR009523; Prokineticin.
                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF182069; AAG16893.2; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL, AF333025; AAK49919.1; -. HSSP; P25687; 11MT. Genew; HGNC:18455; PROK2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 AA; 14314 MW;
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STRAIN-C57BL/6J; TISSUB=Testis;
MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
                                                                                                                                                                                                                                                                                                                                                           1 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP
                                                                                                                                                                                                                                                                                                                                                                                   28 AVITGACDRDPQCGGGMCCAVSLWVKSIRICTPMGKVGDSCHPWIRKVPFLGRRWHHTCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=129/Sv;
MEDLINE=20047850; PubMed=10580115; DOI=10.1016/S0014-5793(99)01473-8;
Wechselberger C., Puglisi R., Lepperdinger G., Boitani C., Kreil G.;
"The mammalian homologue of Bv8 from frog skin is mainly expressed in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bermak J.C., Belluzzi J., Weaver D.R., Leslie F.M., Zhou Q.-Y., Perkineticin 2 transmits the behavioural circadian rhythm of the suprachiasmatic nucleus.";
                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=129/SvJ;
PubMed=11054548; DOI=10.1016/S0378-1119(00)00355-3;
yilok A., Engel B., Beier D., Lepperdinger G.;
"Murine Bv8 gene maps near a synteny breakpoint of mouse chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Name=Prok2; Synonyms=Bv8;
Was musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                       TISSUE=Testis;
MEDLINE=22612805; PubMed=12728244; DO1=10.1038/sj.embor.embor830;
MEDLINE=22612805; PubMed=12728244; DO1=10.1038/sj.embor.embor830;
"The AVIT protein family";
EMBO. Rep. 4:469-473(2003).
EMBL, AVIT925S8; AAP31907.1; -.
HSSP: P55687; ILMT.
InterPro; IPR009523; Prokineticin.
Pfam; PF06607; Prokineticin; 1.
SEQUENCE 108 AA; 11672 MW; C00410399A9B215E CRC64;
                                                                                                                                                                                                                                                                                                                      ö
                                                                                                                                                                                                                                                                          Length 108;
                                                                                                                                                                                                                                                                                                                    Indels
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MEDLINE=22022134; PubMed=12024206; DOI=10.1038/417405a;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QQQXU7; QQQXU5; QQQXU6;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-UJL-2004 (Rel. 44, Last annotation update)
Prokineticin 2 precursor (PK2) (Protein BV8 homolog).
                                                                                                                                                                                                                                                                                                                    4
                                                                                                                                                                                                                                                                          92.4%; Score 426; DB 2; 88.9%; Pred. No. 1.2e-39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. (ISOFORM 2), AND FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    128 AA.
                                                                                                                                                                                                                                                                                                                      5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORMS 1; 2 AND 3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 CLPGLACLRISFNRFICLAOK 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         permatocytes.";
FBBS Lett. 462:177-181(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                      72; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and human 3p21.";
Gene 256:189-195(2000)
                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=10090;
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement ($\frac{4}{9}\end{9}\text{ http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
RA Blake J.A., Bradt D., Brusic V., Chothid C., Corbani L.E., Cousins S., RA Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S., RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J., Aratimond S., Gustinoidh S., Hirokawa N., Jackson I.J., Jarvis E.D., RA Kanai A., Kawasawa Y., Kedzierski R.M., King B.L., RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H., RA Nagashima T., Wumata K., Okido T., Pavan W.J., Pertea G., Pesole G., Ravasi T., Reed J.C., Reid J., Ramachandran S., Rawasi T., Reed J.C., Reid J., Ring B.Z., Ringwald M., Rawasi T., Reed J.C., Reid J., Sandelin A., Schneider C., Sample C.A., Setou M., Shimada K., Asharin R., Wahlestedt C., Sangle C.A., Satou M., Shimada W., A. Verardo R., Wapner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C., Wang I., Yang L., A. Verardo R., Wanshaw-Boris A., Yanagisawa M., Yang I., Yang L., A. Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Sakaume N., Sakot K., Shiraki T., Waki K., Kawai J., Alzawa K., Arakawa T., Fukuda S., A. Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I., Andranichi A., Sakaki K., Sasaki D., Shibete R., Shinagawa R., Andranichi A., Sakaki K., Sasaki D., Shibete R., Sanai, Fundanichi A., Sanai, J., Maraner R., Janai, R., Shibete R., Shinagawa R., Andranichi A., Sakaki K., Sasaki D., Shibete R., Shinagawa R., Andranichi A., Sakaki K., Sasaki D., Shibete R., Shinagawa R., Andranichi A., Sakaki K., Sasaki D., Shibete R., Shinagawa R., Andranichi A., Sakaki K., Sasaki D., Shibete R., Shinagawa R., Andranichi A., Sakaki K., Sasaki D., Shibete R., Shinagawa R., Andranichi A., Sakaki K., Sasaki D., Shibete R., Shinagawa R., Andranichi A., Sakaki K., Sasaki D., Shibete R., Shinagawa R., Andranichi A., Shinagawa R., Andranichi A., Sakaki K., Sasaki D., Shibete R., Shinagawa R., Shina
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BUNDICTION: ACTAGE: Expressed in mid-late pachytene spermatocytes at the stages VII, VIII and IX of the semiferous epithelial cycle. INDUCTION: Activated by CLOCK and BMAL1 heterodimers and light; inhibited by period genes (PER1, PER2 and PER3) and cryptochrome genes (CRX1 and CRX2).

SIMILARITY: Belongs to the prokinecitin family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J., Birney E., Hayashizaki Y.; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nature 420:563-573(2002).

-!- FUNCTION: May function as an output molecule from the suprachiaematic nucleus (SCN) that transmits behavioral circadian rhythm. May also function locally within the SCN to synchronize output. Potently contracts gastrointestinal (GI) smooth muscle (By
                                         Cousins S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 receptor binding; ISS
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GO:0001664; F:G-protein-coupled recept
GO:000187; P:activation of MARK; 1SS.
GO:0001255; P:angiogenesis; 1SS.
GO:0006916; P:anti-apoptosis; 1SS.
GO:0008283; P:cell proliferation; 1SS.
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IsoId=Q9QXU7-2; Sequence=VSP_005220;
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IsoId=Q9QXU7-1; Sequence=Displayed;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AF182068; AAG09439.1; -.
EMBL; AF182067; AAG09439.1; JOINED.
EMBL; AF487280; AAM49572.1; -.
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SUBCELLULAR LOCATION: Secreted.
ALTERNATIVE PRODUCTS:
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EMBL; AF182065; AAF15260.1; -.
EMBL; AF182066; AAF15261.1; -.
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MGD; MGI:1354178; Prok2.
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE-Testis;
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                                                                                                                                                                                                                                                                                                                                                                               Bovinae; Bog.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
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                                                           RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           27 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGQVGDSCHPLTRKSHVANGRQERRRA 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FIId=VSP 005220.
SHVANGRQERRRAKRRKKEVPFWGRRMHHTCPCLPGLAC
LRTSFNRFICLARK -> VSVCTGILGVPSH (in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       27 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGQVGDSCHPLTRKSHVANGRQERRRA
GO; GO:0006935; P:chemotaxis; ISS.
GO; GO:0006723; P:circadian rhythm; IDA.
GO; GO:0007204; P:cytosolic calcium ion concentration elevation; ISS.
GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; I
GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; I
GO; GO:0007186; P:G-protein coupled receptor protein signalin. .; I
GO; GO:0019233; P:perception of pain; ISS.
GO; GO:0045987; P:positive regulation of smooth muscle contra. .; I
InterPro; IPR005523; P:permatogenesis; ISS.
Prokineticin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
NCBI_TaxID=10116;
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STRAIN=Sprague-Dawley;
Chen J. Sutton S., Kuei C., Wilson S.J., Lovenberg T.W., Liu C.;
Submitted (JUL-2003) to the EMBL/GenBank/DDBJ databases.
EMBL, AY348322, AAR06524.1;
InterPro: IPR009523; Prokineticin.
Pfam; PF06607; Prokineticin.
SEQUENCE 128 AA; 14223 MW; 67050CCIA7D59466 CRC64;
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                                                                                                                                                                                                                                                                                        Alternative splicing, Biological rhythms; Neuropeptide, Signal.
SIGNAL 1 26 Potential.
CHAIN 27 128 Prokineticin 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 128;
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SF08BA177FDDB58C CRC64;
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By similarity.
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By similarity.
Missing (in isoform 2).
/FTIG-VSP_005220.
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Last annotation update)
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Pred. No. 2.1e-39;
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Best Local Similarity 75.5.
Best Total 77; Conservative
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128
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94
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DO CÓGV8
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Joubert F.J., Strydom D.J.;
"Snake venom. The amino acid sequence of protein A from Dendroaspis
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30-MAY-2000 (Rel. 39, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Lintestinal toxin 1 (MIT 1) (MIT1) (Venom protein A).
Dendroaspis polylepis polylepis (Black mamba).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Lepidosauria; Squamata; Scleroglossa; Serpentes; Colubroidea; Elapidae; Elapinae; Dendroaspis.
                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
                                                                                                                                                                                                                                                                                                        MEDLINE=22612805; PubMed=12728244; DOI=10.1038/sj.embor.embor830;
SASSER A., WinkImayr M., Lepperdinger G., Kreil G.;
"The AVIT protein family.";
EMBO Rep. 4:469-473 (2003).
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                                     01-JUN-2003 (TrEMBLrel. 24, Created)
01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
BV8/prokineticin 2-like protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88.1%; Score 406; DB 2; 71.3%; Pred. No. 2.3e-37; 7ative 5; Mismatches 4;
128 AA
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PRT;
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PRELIMINARY;
                                                                                                                                 Bos taurus (Bovine).
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105 AA;
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Best Local Similarity
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                                                       endothelium.";
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16-OCT-2001 (Rel. 40, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Prokineticin 1 precursor (Endocrine-gland-derived vascular endothelial growth factor) (EG-VEGF) (Mambakine) (UNQ600/PRO1186).
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                                                                     MEDLINE=20036442; PubMed=10567694; DOI=10.1016/S0014-5793(99)01459-3; Schweitz H., Pascaud P., Diochot S., Moinier D., Lazdunski M.; "MITI, a black mamba toxin with a new and highly potent activity on intestinal contraction."; PEBS Lett. 461:183-188(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1; Gaps
                                                                                                                                                                                                                                           Boisbouvier J., Albrand J.-P., Blackledge M., Jaquinod M., Schweitz H., Lazdunski M., Marion D.;
"A structural homologue of collpase in black mamba venom revealed by MRR floating disulphide bridge analysis.";
J. Mol. Biol. 283:205-219(1998).
-!-FUNCTION: Potently contract gastrointestinal (GI) smooth muscle...
-! SUBCELLULAR LOCATION: Secreted...
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Li M., Bullock C.M., Knauer D.J., Ehlert F.J., Zhou Q.Y.;
"Identification of two prokineticin cDNAs: recombinant proteins
potently contract gastrointestinal smooth muscle.";
Mol. Pharmacol. 59:692-698 (2001).
                                                                                                                                                                                                                               MEDLINE=98437381; PubMed=9761684; DOI=10.1006/jmbi.1998.2057;
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C -> S (in Ref. 1).
S -> C (in Ref. 1).
 polylepis polylepis (black mamba) venom.";
Hoppe-Seyler's Z. Physiol. Chem. 361:1787-1794(1980).
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3D-structure; Direct protein sequencing; Toxin.
DISULFID 7 19
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InterPro; IPR009523; Prokineticin.
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61.7%;
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Best Local Similarity
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                                                           CHARACTERIZATION.
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CONFLICT
SEQUENCE
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Dillard-Telm L., Frantz G., Rangell L., DeGuzman L., Keller G.-A., Peale F., Gurney A., Hillan K.J., Ferrara N.; "Identification of an angiogenic mitogen selective for endocrine gland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=22887296; PubMed=12975309; DOJ=10.1101/gr.1293003; MEDLINE=22887296; PubMed=12975309; DOJ=10.1101/gr.1293003; MEDLINE=22887296; PubMed=12975309; DOJ=10.1101/gr.1293003; Clark H.F., Gurney A.L., Abaya B., Baker K., Baldwin D., Brush J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Baton D., Roster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liso D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Santh V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P., Gray A., The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Protein Sci. 13:2819-2824 (2004).

-I- FUNCTION: Potently contract gastrointestinal (GI) smooth muscle.
-I- FUNCTION: Potently contract gastrointestinal (GI) smooth muscle.
Induces proliferation, migration and fenestration (the formation of membrane discontinuities) in capillary endothelial cells derived from endocrine glands. Has little or no effect on a variety of other endothelial and non-endothelial cell types.
-I- SUBCELMULAR LOCATION: Secreted.
-I- TISSUE SPECIFICITY: Expressed in the steroidogenic glands, ovary, testis, adrenal and placenta.
-I- SIMILARITY: Belongs to the prokinecitin family.
                                                                                                                                                                                                                                                                                                                                         "Mambakine, a snake venom related endocrine hormone that controls
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE OF 20-34.

PubMed=15340161; DOI=10.1110/ps.04682504;
Zhang Z., Henzel W.J.;
"Signal peptide prediction based on analysis of experimentally verified cleavage sites.";
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                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (APR-2001) to the EMBL/GenBank/DDBJ databases.
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Pred. No. 1.2e-24;
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Pfam; PF06607; Prokineticin; 1.
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EMBL, AX028225; AAK33111.1; --
EMBL, AX356683; AAQ89046.1; --
HSSP, P25687; LIMT.
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                                                                                                                                                                                  Nature 412:877-884(2001).
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05-JUL-2004
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Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul R.F., Jordan H., Moore T., Max S.I., Mang J., Hsieh F.,
Battelenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Brownstein M., Soases M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Tooshiyuki S., Carninci P., Frange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKwan P.J., McKernan K.J., Makek J.A., Guararene P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.,
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                                                                          20 AVITGACERDVQCGAGTCCAISLWLRGLRMCTPLGREGEECHPGSHKVPFFRKKHHTCP
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Gaps
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
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18; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Strausberg R., Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE 105 AA; 11729 MW; E570FDE30EFB52D2 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                             105 AA.
14; Mismatches
                                                                                                                                                                                                                                                                                                                                                              Created)
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                                                                                                                                          61 CLPGLACLRISFNRFIC 77
                                                                                                                                                                            CLPNLLCSRFPDGRYRC 96
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HSSP; P25687; 11MT.
45; Conservative
                                                                                                                                                                                                                                                                                                               PRELIMINARY;
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                                                                             (Rel. 42, Last sequence update)
(Rel. 44, Last annotation update)
1 precursor (Endocrine-gland-derived vascular endothelial
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                                                                                                                                                                                                                                                                                                                                                                                                                                   Masuda Y., Takatau Y., Terao Y., Kumano S., Ishibashi Y., Suenaga M., Abe M., Fukusumi S., Watanabe T., Shintani Y., Yamada T., Hinuma S., Inatomi N., Ohtaki T., Onda H., Fujino M., Fukusumi S., Hinuma S., Isolation and identification of Ed-VEGF/prokineticins as cognate ligands for two orphan G-protein-coupled receptors.", Biochem Biochem Biochem Capators. "Salsolation or manual G-protein-coupled receptors.", Induces proliferation, migration and fenestration (the formation of membrane discontinuities) in capillary endothelial cells derived from endocrine glands. Has little or no effect on a variety of other endothelial and non-endothelial cell types (By
                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=Sprague-Dawley;
MEDLINE=22050031; PubMed=12054613; DOI=10.1016/S0006-291X(02)00239-5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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By similarity.
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W, similarity.
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SUBCELLULAR LOCATION: Secreted (By similarity).
SIMILARITY: Belongs to the prokinecitin family.
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01-OCT-2002 (TrEMBLrel. 22, Created)
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Pfam; PF06607; Prokineticin; 1.
Growth factor; Mitogen; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
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HSSP; P25687; 11MT.
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138
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11642 MW;
                                                      10-OCT-2003 (Rel. 42, Created)
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                                                                                                                             precursor
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                                                                                                                                                               growth factor) (EG-VEGF)
STANDARD;
                                                                                                                                                                                                                   Rattus norvegicus (Rat)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RGD: 620898; Prok1
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                        NCBI_TaxID=10116;
                                                                                                                                      Prokineticin 1
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Q8K457
ID Q8K45
AC Q8K45
DT 01-OC
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96 AA
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                          entities requires a license agreement (9¢
or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                              Protein
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                                                                                                       EMBL; AF168790; AAD45816.1; -.
HSSP, P25687; 11MT.
InterPro; IPR009523; Prokineticin.
Pfam; PF06607; Prokineticin; 1.
Direct protein sequencing; Signal.
SIGNAL
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80 CKSGLTCSK-SGEKFQC 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   42; Conservative
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
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DISULFID
SEQUENCE
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Q8JFQ0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
TISSUB=Skin secretion;
MEDLINB=99349621; PubMed=10422759; DOI=10.1016/S0014-2999(99)00229-0;
MEDLINB=9349621; PubMed=10422759; DOI=10.1016/S0014-2999(99)00229-0;
MEDLINB=9349621; PubMed=10422759; DOI=10.1016/S0014-2999(99)00229-0;
MEDLING WE HORSELD FROM GROUP OF WELL OF WELL
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                       STRAIN=C57BL/6;
MEDLINE=2202134; PubMed=12024206; DOI=10.1038/417405a;
Cheng M.Y., Bullock C.M., Li C., Lee A.G., Bermak J.C., Belluzzi J.,
Weaver D.R., Leelie F.M., Zhou Q.Y.;
"Prokineticin 2 transmits the behavioural circadian rhythm of the
suprachiamentic mucleus.";
                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 417:405-410(2002).
Nature 417:405-410(2002).
BENBL; AF487281; AAM49573.1; -.
HSSP; P2587; IIMT.
MGD; MG1:2180370; Prok1.
MGO; GO:0000187; P:activation of MAPK; IDA.
GO; GO:000187; P:activation of MAPK; IDA.
GO; GO:0001881; P:activation of MAPK; IDA.
GO; GO:0001884; P:positive regulation of cell proliferation; IDA.
GO; GO:0045765; P:regulation of angiogenesis; IDA.
InterPro; IPR009523; Prokineticin.
PFem; PF06607; Prokineticin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         81 AA; 9192 MW; 7BBE3EC6B16A8011 CRC64;
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--- SUBCELLULAR LOCATION; Secreted.
--- SIMILARITY: Belongs to the prokinecitin family.
        Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 40, Created)
     01-OCT-2002 (TrEMBLrel. 22, 01-MR-2004 (TrEMBLrel. 26, Prokineticin I (Fragment). Name-Proki; Synonyms-Pki; Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 LČSŘFPDGŘYRC 72
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein Bv8 precursor.
                                                                                                                                                                                                                                                             SEQUENCE FROM N. A.
                                                                                                                                                                                                     NCBI_TaxID=10090;
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16-OCT-2001
05-JUL-2004
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Q9PW66;
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Pfam, P.
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modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.lsb-sib.ch/announce/
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MEDIINE-2215112; Pubmed-112628181; DOI=10.1016/S1096-4959(02)00294-4;
Inl H., Liu H., Lee W.H., Zhang Y.,
Try novel Bv8-like peptides from skin secretions of the toad Bombina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AVITGACDKDSQCGGGGCGAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP
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Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
Bukaryota, Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Archeobatrachia; Bombina.
NCBI_TaxID=161274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 134:509-514(2003).
EMBL: AF411091; AAN03822.1; -.
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By similarity.
By similarity.
By similarity.
By similarity.
By similarity.
A12490A7437609B4 CRC64;
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InterPro; IPR009523; Prokineticin.
Pfam; PF06607; Prokineticin; 1.
SEQUENCE 96 AA; 10198 MW; EC4EAA5EFB49B2F0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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53.2%; Pred. No. 9.7e-20;
ive 12; Mismatches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 248.5; DB 1
Pred. No. 5.7e-20;
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Gaps

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20 AVITGVCDRDAQCGSGTCCAASAFSRNVRFCVPLGNNGEECHPASHKVPYNGKRLSSLCP 79
                                                                                                                                                                                                                                 20 AVITGVCDRDAQCGSGTCCAASAFSRNIRFCVPLGNNGEECHPASHKVPYNGKRLSSLCP
                                                                                                                                                                                              1 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP
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Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BM8-c protein precursor.
Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chen T., Farragher S., Bjourson A.J., Orr D.F., Rao P., Shaw "Granular gland transcriptomes in stimulated amphibian skin
                                                                       50.4%; Score 232.5; DB 2; Length 96; 50.6%; Pred. No. 3.4e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 2; Length 96;
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Chen T., Farragher S., Bjourson A.J., Orr D.F., Rao P., Shaw
"Granular gland transcriptomes in stimulated amphibian skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   24; Indels
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BM8-c protein.
227EAIA5C49B18A6 CRC64;
                  96 AA; 10127 MW; 226A65C8654B1BA6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 22, Created)
(TrEMBLrel. 22, Last sequence update)
(TrEMBLrel. 26, Last annotation update)
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49.4%; Pred. No. 3.4e-18;
tive 14; Mismatches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96 AA
                                                                                                                                   13, Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2002 (TrEMBLrel. 22, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro, IPR009523; Prokineticin. Pfam; PF06607; Prokineticin; 1. Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Biochem. 371:125-130(2003).
EMBL; AJ440232; CAD29342.1; -.
HSSP; P25687; IIMT.
                                                                                                                                                                                                                                                                                                                  61 CLPGLACLRISFNRFIC 77
                                                                                                                                                                                                                                                                                                                                                                          80 CNTGLTCPK-SGEKFQC 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 CLPGLACLRTSFNRFIC 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 CNTGLTCSK-SGEKFOC 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20 96
96 AA; 10103 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity 49.4%
nes 38; Conservative
                                                                                                                                      39; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BM8-d protein precursor.
                                                                                                       Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=161274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=161274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            secretions.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-OCT-2002
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-OCT-2002
01-MAR-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                  SEQUENCE
                                                                              Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            QBJFY0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QBJFY0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q8JFY1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Q8JFY0
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01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
05-JUL-2004 (TrEMBLrel. 22, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
BM8-a protein precursor (Bv8 protein homolog 1).
BM8-a protein grecursor (Bv8 protein homolog 1).
Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Archeobatrachia; Bombina.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Skin secretions;
MEDLINE=22515712; PubMed=12628381; DOI=10.1016/S1096-4959(02)00294-4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Lai R., Liu H., Lee W.H., Zhang Y.; "Two novel Bv8-like peptides from skin secretions of the toad Bombina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
BM8-e protein precursor.
Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Archeobatrachia; Bombina.
NCBI_TaxID=161274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chen T., Farragher S., Bjourson A.J., Orr D.F., Rao P., Shaw C., "Granular gland transcriptomes in stimulated amphibian skin
                                                                                                                                                                                                                                                                                                                                                                          Chen T., Farragher S., Bjourson A.J., Orr D.F., Rao P., Shaw C., "Granular gland transcriptomes in stimulated amphibian skin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Comp. Biochem. Physiol. B, Biochem. Mol. Biol. 134:509-514(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.7%; Score 233.5; DB 2; Length 96; 50.6%; Pred. No. 2.7e-18; ive 13; Mismatches 24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BM8-a protein.
2269AAC8654B18A6 CRC64;
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BM8-e protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Potential
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     J. Biochem. 371:125-130(2003).
EMBL; AJ440234; CAD29344.1; -
HSSP; P25687; IIMT.
InterPro; IPR009523; Prokineticin.
Pfam; PF06607; Prokineticin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EMBL; AJ440230; CAD29340.1; -.
EMBL; AF411090; AAN03821.1; -.
HSSP; P25687; IIMT.
IILCEPTO; IPR09523; Prokineticin.
Pfam; PF06607; Prokineticin; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80 CNTGLTCSK-SGEKFQC 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 CLPGLACLRTSFNRFIC 77
                                                                                                                                                                                                                                                                                                                                                                                                                                               sretions.";
Biochem. 371:125-130(2003)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 AA; 10117 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local Similarity 50.64
hes 39, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19
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TISSUE=Skin;
                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                 TISSUE=Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      maxima.";
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SIGNAL
CHAIN
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Q8JFX9
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN=CZECH II, TISSUE=Mammary tumor;

MEDIINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

X Altschul S.F., Zeberg B. Buerow K.H., Schaefer C.F., Barlar N.K.,

Altschul S.F., Zeberg B. B. Buerow K.H., Schaefer C.F., Barlar N.K.,

A pitchins R.F., Jordan H., Moore T., Max J.I., Mang J., Haishe F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

A pitchins R.F., Jordan H., Moore T.C., Mang J., Haishe F.,

Stapleton M.J., Uddin T.B., Tochiyuki J., Carninci P., Prange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raba S.S., McZwan P.J., McKernan R.J., Malke J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

XA Richards S., Worley K.C., Hale S., Garcia A.M., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

A Raciguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,

A Gones S.J., Marra M.A.,

A Gones C. Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

A Gones S.J., Marra M.A.,

A Go
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP
               Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleóstomi, Amphibia; Batrachia, Anura, Archeobatrachia, Bombinatoridae, Bombina NCBI_TaxID=161274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad)
                                                                                                                                                                                                                                                                                                                                                                                                        Query Match

47.4%; Score 218.5; DB 2; Length 96;
Best Local Similarity 48.1%; Pred. No. 1.2e-16;
Matches 37; Conservative 14; Mismatches 25; Indels
                                                                                                                                Chen T., Farragher S., Bjourson A.J., Orr D.F., Rao P., Shar
"Granular gland transcriptomes in stimulated amphibian skin
                                                                                                                                                                                                                                                                                                                                            BM8-b protein.
D77CAACFF54B020C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Last sequende update)
Last annotation update)
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                                                                                                                                                                                                                                                                                                                               Potential.
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STRAIN-CZECH II; TISSUE-Mammary tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                 J. Biochem. 371:125-130(2003).
EMBL; AJ440231; CAD29341.1; -.
HSSP; P25687; IIMT.
InterPro; IPR009523; Prokineticin.
Pfam; PF06607; Prokineticin; 1.
                                                                                                                                                                                                                                                                                                                                                                      96 AA; 10186 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 CLPGLACLRTSFNRFIC 77
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20,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2002 (TrEMBLrel. 01-MAR-2002 (TrEMBLrel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dickkopf homolog 4.
                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=10090;
                                                                                                                                                                                    secretions.";
                                                                                                                        TISSUE=Skin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Name=Dkk4;
                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                          Signal.
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                                                                                                                                                                                                                                                                                                                                      20 AVITGVCDRDAQCGSGTCCAASAFSRNIRFCVPLGNNGEECHPASHKVPYNGKRLSSLCP 79
                                                                                                                                                                                                                                                                                                            1 AVITGACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BM8-f protein precursor.

Bombina maxima (Giant fire-bellied toad) (Chinese red belly toad).

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Amphibia; Batrachia; Anura; Archeobatrachia; Bombinatoridae; Bombina.

NCBI_TaxID=161274;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chen T., Farragher S., Bjourson A.J., Orr D.F., Rao P., Shaw C., "Granular gland transcriptomes in stimulated amphibian skin
                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      48.9%; Score 225.5; DB 2; Length 96; 49.4%; Pred. No. 2.1e-17; Live 13; Mismatches 25; Indels 1
                                                                                                                                                                                                                            ch 49.9%; Score 230; DB 2; Length 96; 1. Similarity 51.4%; Pred. No. 6.5e-18; 36; Conservative 13; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BM8-f protein.
2269A070FFE118A6 CRC64;
                                                                                                                                             Potential.
BM8-d protein.
2269AAD4154B18A6 CRC64;
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Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-2002 (TrEMBLrel. 22, Created)
01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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EMBL, AJ440235; CAD29345.1; -.
HSSP; P25687; IIMT.
Interpro; IPR009523; Prokineticin.
Pfam; PF06607; Prokineticin; 1.
                       J. Biochem. 371:125-130(2003).
EMBL; AJ440233; CAD29343.1; -..
EMSP; PS5687; IIMT.
InterPro; IPR09523; Prokineticin.
Pfam; PF06607; Prokineticin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  96 AA; 10058 MW;
                                                                                                                                                 1 19
20 96
96 AA; 10057 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                    61 CLPGLACLRT 70
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CNTGLTCSKS 89
                                                                                                                                                                                                                                 Query Match
Best Local Similarity
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                                                                                                                                                                         CHAIN
SEQUENCE
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                                                                                                                                Signal.
SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QBJFX8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 18
Q8JFX8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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EMBL; AF030433; AAC02426.1; -.
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01-JUN-2003 (TrEMBLrel. 24,
01-MAR-2004 (TrEMBLrel. 26,
                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                             141
269
262
                                 Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                          272 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
es 24; Conser
                                                                                                                                                                                                                                                                                       HSSP; P25687; 11MT
                                                                                     SEQUENCE FROM N.A.
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                                                                NCBI_TaxID=10090;
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CARBOHYD
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Matches
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                                                                                                                                                  6 ACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSC----HPLTRKVPFFGRRMHHTCPC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20 CIRSSDCAAGLCCARHFWSK---ICKPVIREGQVCTRHRRK-GAHGLEIFQRCPCAEGMA 75
                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=21559221; PubMed=11702953; DOI=10.1016/S1534-5807(01)00041-7; Mukhopadhyay M., Shtrom S., Rodriguez-Esteban C., Chen L., Tsukui T., Gomer L., Dorward D.W., Glinka A., Grinberg A., Huang S.P., Niehrs C.,
                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7 CDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCPCLPGLA
                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4; Gaps
                                                                                                                   11;
                                                                                         Query Match 24.4%; Score 112.5; DB 2; Length 221; Best Local Similarity 37.9%; Pred. No. 0.00016; Matches 25; Conservative 7; Mismatches 23; Indels 11
                                                                                                                                                                                                                                                                                                                                                                                                                         Gomer L., Dorwara D.m., Carrell Belmonte J.C.I., Westphal H.;
Polickkopfi is required for embryonic head induction and limb morphogenesis in the mouse.";
morphogenesis in the mouse.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 96;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               28; Indels
Strausberg R.; Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases. EMBL; BC018400; AAH18400.1; -. HSSP; P25687; IIMT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tsukui T., Belmonte J.C.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AYO49017; AALO7515.1; --
HSSP; P25687; 11MT.
                                          MGD; MGI:2385299; Dkk4.
GO: 60:0005615; C:extracellular space; TAS.
Pfam; PF04706; Dickkopf N; 1.
SEQUENCE 221 AA; 24260 MW; 670AD9F750BF1715 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      043E6A647D5AF4E7 CRC64;
                                                                                                                                                                                                                                                                                      Last sequence update)
Last annotation update)
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Pred. No. 0.00014;
                                                                                                                                                                                                                                                         96 AA
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(Rel. 40, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              6; Mismatches
                                                                                                                                                                                                                                                                            Created)
                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      96 AA; 10756 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           23.9%;
                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 37.77
Best Local Similarity 37.77
Conservative
                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                                                                                                               Gallus gallus (Chicken).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                     197 GPGLTC 202
                                                                                                                                                                                 62 LPGLAC 67
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                        Dkk-1 (Fragment).
Name=Dkk-1;
                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9031;
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DKKI MOUSE
ID DKKI MOUSE
AC 054908;
DT 16-0CT-2001 (
DT 16-0CT-2001 (
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                                                                                                                                                                                                                                    RESULT 21
Q8UUX3
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                                                                                                                                                                                                                                                                                                          7 CDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCPCLPGLA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:1329040; Dkkl.
InterPro; IPR006796; dickkopf_N.
Pfam; PF04706; Dickkopf_N; 1.
Developmental protein; Glycoprotein; Sighal; Wnt signaling pathway.
05-JUL-2004 (Rel. 44, Last annotation update)
Dickkopf related protein-1 precursor (Dkk-1) (Dickkopf-1) (mDkk-1)
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Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                  Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           31 Potential.
272 Dickkopf related protein-1.
141 DKK-type Cyb-1.
262 N-linked (GlcNAc. .) (Pot-
29268 MW, AB9FA35DFA57D3EE CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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197 GPGLLC 202
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DOMAIN
CONFLICT
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Q9PWH3
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Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
M. Bronstein M.J., Uddin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalon D.K., Muzny D.M., Sodergene E.J., Lu X., Gibbs R.A.,
Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Boutfard G.G.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
X. Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
Jones S.J., Marra M.A.;
M. Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                         7 CDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCPCLPGLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=20035735; PubMed=10570958; DOI=10.1016/S0378-1119(99)00365-0; Krupnik V.B., Sharp J.D., Jiang C., Robison K., Chickering T.W., Amaravadi L., Brown D.E., Guyot D., Mays G., Leiby K., Chang B.D., Duong T., Goodearl A.D., Gearing D.P., Sokol S.Y., McCarthy S.A.; "Functional and structural diversity of the human Dickkopf gene
                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                09UBT3, 09Y4C3,
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Dickkopf related protein-4 precursor (Dkk-4) (Dickkopf-4)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                         STRAIN=B5/EGFP transgenic ICR mice; TISSUE=Trophoblast Stem Cell;
                                                                                                                                                                                                                                                                                                                                                                                                                 4,
                                                                                                                                                                                                                                                                                                                                                                                     22.3%; Score 103; DB 2; Length 272; 39.3%; Pred. No. 0.0022;
                                                                                                                                                                                                                                                                                                                                                                                                                29; Indels
                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (APR-2003) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                         MGD; MGI:1329040; Dkkl.
GO; GO:0005615; C:extracellular space; TAS.
InterPro; IPR06796; dickkopf_N.
Pfam; PF04706; Dickkopf_N; ADFAC3E7B8859A9E CRC64;
SEQUENCE 272 AA; 29297 MW; ADFAC3E7B8859A9E CRC64;
                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Tate G., Suzuki T., Mitsuya T.,
                                                                                                                                                                                                                                                                                 EMBL; BC050189; AAH50189.1;
HSSP; P25687; 11MT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD; ·
                                                                                                                                                                                                                                                                                                                                                                                                                  24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene 238:301-313(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tate G., Mitsuya T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251 ¢ 251
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=DKK4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 family.'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DKK4_HUMAN
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/anflounce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6 ACDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSC----HPLTRKVPFFGRRMHHTCPC 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            . .; NAS.
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Brachydanio metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
NCBI_TaxID=7955;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                    Protein Sci. 13:2819-2824(2004).
-!- FUNCTION: Inhibitor of Wnt signaling pathway.
-!- SUBCELLULAR LOCATION: Secreted.
-!- SUBCELLULAR LOCATION: Expressed in cerebellum, T-cells, esophagus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Dickkopf rélated protein-4.
Dickkopf rélated protein-4 short form.
DKK-type Cys-1.
                                                                                                                                                                                                                                                                                                                                                                                        furin-like protease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MIM; 605417; -.
GO; GO:0030178; P:negative regulation of Wnt receptor signali.
InterPro; IPR006796; dickkopf_N.
                                                                                                                                            "Signal peptide prediction based on analysis of experimentally verified cleavage sites.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 101.5; DB 1; Length 224; Pred. No. 0.0027; 6; Mismatches 25; Indels 11.
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Pfam; PF04706; Dickkopf N; 1.
Developmental protein; Direct protein sequencing; Signal;
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DKK-type Cys-2.
M -> L (in Ref. 3).
45F8EBC476961357 CRC64;
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                            -!- PTM: Appears to be not glycosylated.
-!- PTM: Can be proteolytically processed by a f
-!- SIMILARITY: Belongs to the dickkopf family.
                                                                                    PubMed=15340161; DOI=10.1110/ps.04682504;
Zhang Z., Henzel W.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; AF177397; AAF02677.1; -... EMBL; AB018005; BAA33475.1; -... EMBL; AB018004; BAA33475.1; JOINED. EMBL; AB018004; BAA33475.1; JOINED. EMBL; AB017788; BAA33438.1; -... HSSP; PZ5687; IIMT. Genew; HGNC: 2894; DKK4.
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93 M
24875 MW;
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1 Similarity 36.4%;
24; Conservative
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01-MAY-2000 (TrEMBLrel. 13,
01-MAR-2003 (TrEMBLrel. 23,
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Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AB023488; BAA82135.1; -.
ZETN; ZDB-GENB-990708-5; dkk1.
GO; GO:0007277; P:develpoment; IEA.
GO; GO:0007277; P:develpoment; IEA.
GO; GO:0030178; P:negative regulation of Wnt receptor signali. .; IEA.
InterPro; IPR006796; dickkopf.N.
Pfam; PF04706; Dickkopf.N; 1.
SEQUENCE 240 AA; 25985 MW; AA6CF04C5901AB12 CRC64;
                                                                                                                                                                                        7 CDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCPCLPGLA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Roessler E., Du Y., Glinka A., Dutra A., Niehrs C., Muenke M.; "The genomic structure, chromosome location, and analysis of the human DKK1 head inducer gene a candidate for holoprosencephaly."; Cytogenet. Cell Genet. 89:220-224(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
TISSUE=Fetal kidney;
MEDLINE=20035735; PubMed=10570958; DOI=10.1016/S0378-1119(99)00365-0;
                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Krupnik V.E., Sharp J.D., Jiang C., Robison K., Chickering T.W., Amaravadi L., Brown D.E., Guyot D., Mays G., Leiby K., Chang B., Duong T., Goodearl A.D.J., Gearing D.P., Sokol S.Y., McCarthy S.A., "Functional and structural diversity of the human Dickkopf gene
                                                                                                                                                                                                                                                                                                                                           16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Dickkopf related protein-1 precursor (Dkk-1) (Dickkopf-1) (hDkk-1)
(SK) (UNQ492/PRO1008).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003;
Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,
                                                                                                                                                                                                                                                                                                                                                                                                                             Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
TISSUB-Letenyosarcoma;
MEDLINE-9931500. PubMed=10383463; DOI=10.1074/jbc.274.27.19465;
MEDLINE-99315co A., Nieto Soria A., Burgess W.H., Miki T.,
Bottaro D.P., Kraus M.H., Aaronson S.A.;
"Isolation and biochemical characterization of the human Dkk-1 homologue, a novel inhibitor of mammalian Wnt signaling.";
                                                                                                                                                                   4 ;
                                                                                                                                        Query Match 21.7%; Score 100; DB 2; Length 240; Best Local Similarity 37.7%; Pred. No. 0.0043; Matches 23; Conservative 5; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tate G., Suzuki T., Mitsuya T.;
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                        266 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
MEDLINE=20422487; PubMed=10965128;
                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene 238:301-313(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
Tate G., Suzuki T.,
 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=9606;
                                                                                                                                                                                                                                                             220 C 220
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                                                                                                                                                                                                                                                                                                                      DKK1 HUMAN
094907;
                                                                                                                                                                                                                                                                                                                                                                                                       Name=DKK1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    family
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NEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Altashul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B. Buetow K.H., Schaefer C.F., Bhat N.K.,
Aptachench L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Rab Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J. Usdin T.B., Torshiyuki S., Carninci P., Prange C.,
Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Bosak S.A., McKwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Rabey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Brown R. M., Schein J.E., Jones S.J.M., Marza M.A.;
Bromeration and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                      effort to identify novel human secreted and transmembrane proteins: a
                                                                                                                                                                                                                                                å
Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd Baton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie B., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watenabe C., Wieand D., Woods K., Xie M.-H., Yansura D. Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P., Gray A.;

"The secreted protein discovery initiative (SPDI), a large-scale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    min, 502.123;
GO; GO:0008083;
F:growth factor activity; TAS.
GO; GO:0004871; F:signal transducer activity; TAS.
InterPro; IFR066796; dickkopf.
Pfam; PF04706; Dickkopf. N;
Developmental protein; Direct protein sequencing; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PubMed=15340161; DOI=10.1110/ps.04682504;
Zhang Z., Henzel W.J.;
"Signal peptide prediction based on analysis of experimentally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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-!- FUNCTION: Inhibitor of Wht signaling pathway.
-!- SUBCELLULAR LOCATION: Secreted.
-!- TISSUE SPECIFICITY: Placenta.
-!- SIMILARITY: Belongs to the dickkopf family.
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EMBL, AF177394; AAF02674.1; --
EMBL, AB020315; BAA34651.1; --
EMBL, AB020314; BAA34651.1; --
EMBL, AF261158; AAG15544.1; --
EMBL, AF261157; AAG15544.1; --
EMBL, AF261157; AAG15541.1; --
EMBL, BC001539; AAH01539.1; --
HSSP, PZ6687; 11MT.
Genew; HGNC:2891; DKK1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            bioinformatics assessment.";
Genome Res. 13:2265-2270(2003).
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musculus (Mouse).
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les 22; Conserv
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                                     NCBI_TaxID=10090;
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                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCPCLPGLA 66
                                                                                                                7 CDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCPCLPGLA 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Dickkopf related protein-2 precursor (Dkk-2) (Dickkopf-2) (mDkk-2).
                                                                                                                                                                                                                                                                                        Xenocommus, African clawed frog).
Sukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
                             DKK-type Cys-1.
DKK-type Cys-2.
DKK-type Cys-2.
NK-linked (GlckAc. . .) (Potential).
5E878B2CCE4236BA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                 GO; GO:0005576; C:extracellular; IEA.
GO; GO:0007275; P:development; IEA.
GO; GO:0007275; P:development; IEA.
InterPro; IPR006796; dickkopf_N.
InterPro; IPR011052; Prot_any__inhib.
Pfam; PF04706; Dickkopf_N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4,
                                                                       Score 100; DB 1; Length 266;
Pred. No. 0.0047;
5; Mismatches 29; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 255;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            21.5%; Score 99; DB 2; Length 255
36.1%; Pred. No. 0.0059;
tive 6; Mismatches 29; IndelB
                                                                                                                                                                                                                                                                                                                                                          Wu W., Glinka A., Delius H., Niehrs C.;
Submitted (NOV-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ300197; CAC17815.1; -.
HSSP; P25687; 11MT.
                     Dickkopf related protein-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Potential.
dickkopf2.
; F270B7DD0F4FCD73 CRC64;
                                                                                                                                                                                                                                                    Last sequence update)
Last annotation update)
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                                                                                                                                                                                                                                             Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 29 P
30 255 d
255 AA; 28096, MW;
   pathway.
                                                          28671 MW;
                                                                           Query Match 21.7%;
Best Local Similarity 37.7%;
Matches 23; Conservative
                                                                                                                                                                                                                                             16,
16,
23,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity 36.1
nes 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                                            01-MAR-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                      01-MAR-2001 (TrEMBLrel.
01-MAR-2003 (TrEMBLrel.
                     266
138
263
256
    Signal; Wnt signaling SIGNAL 1 31
                                                                                                                                                                                                                                                                                                                        Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                          Dickkopf2 precursor.
                     32
85
189
256
266 AA;
                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Q9QYZ8;
                             DOMAIN
DOMAIN
CARBOHYD
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
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                                                                                                                                                                                                                                    Q9DDA4;
                                                                                                                                                                                                                           Q9DDA4
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage, by, and for connectal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             noved. Usage by and for commercial (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 CDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCPCLPGLA 66
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05-JUL-2004 (TTEMBLEEL: 27, Last annotation update)
Mus musculus 10, 11 days embryo whole bddy cDNA, RIKEN full-length
enriched library, clone:2810421D01 product:DICKKOPF RELATED PROTEIN-2
(DKK-2) (DICKKOPF-2) (MDKX-2) homolog (Mus musculus 11 days embryo
head cDNA, RIKEN full-length enriched library, clone:6230401K18
product:DICKKOPF RELATED PROTEIN-2 (DKK-2) (DICKKOPF-2) (MDKK-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-C57BL/67; TISSUE-Head, and Whole body;
MEDLINE-99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
Carninci P., Hayashizaki Y.;
                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MGD, MGI:1890663; Dkk2.
Interpro; IPRO06796; dickkopf_N.
Pfam; PPO4706; Dickkopf_N; 1.
Developmental protein; Glycoprotein; Signal; Wnt signaling pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52 N-linked (GlcNac. . .) (Potential) 28416 MW; EAAB76F2D2C9780D CRC64;
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DKK-type Cys-2.
N-linked (GlcNAC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (Se
or send an email to license@isb-sib.ch).
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259 AA;
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SEQUENCE FROM N.A.

Adadani J., Alzawa K., Akimuza T., Arakawa T., Bono H., Carninci P., Adachi J., Alzawa K., Akimuza T., Hara A., Hashizume W.,

Huyashida K., Hayatsu N., Hiramoto K., Hiraoka T., Hirozane T.,

Hori F., Indtani K., Ishii Y., Itoh M., Kagawa I., Kaukawa T.,

Katoh H., Kawai J., Kojima Y., Kondo S., Konno H., Kouda M., Koya S.,

Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,

Nishi K., Nomura K., Numazaki R., Ohno M., Ohsato N., Okazaki Y.,

Saito R., Saitoh H., Sakai C., Sakai K., Sakazume N., Sano H.,

Sasaki D., Shibata K., Shinagawa A., Shiraki T., Sogabe Y., Tanaka T.,

Tagawa A., Toya T., Yasunii shi A., Muramatsu M., Hayashizaki Y.;

Tumaru A., Toya T., Yasunii shi A., Muramatsu M., Hayashizaki Y.;

Submitted (UUL-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; AK028225; BAC25824.1; -.

PERBL; AK0281749; BAC25536.1; -.
                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
STRALN=C57BL/64; TISSUE=Head, and Whole body;
MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
Carninci P., Shibata Y., Hayatsu N., Sugahara Y., Shibata K., Itoh M.,
Konno H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
Wormalization and subbraction of cap-trapper-selected cDNAs to
prepare full-length cDNA libraries for rapid discovery of new genes.";
Genome Res. 10:1617-1630(2000).
                                                                                                                                                                                                                                  the RIKEN Genome Exploration Research Group Phase I & II Team; "Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs."; Nature 420:563-573 (2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN—CSTBL/60; TIESUE=Head, and Whole body;
MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
Shibata K., Itoh M., Aizawa K., Nagaoka S., Sasakh N., Carninci P., Suman A., Akiyama J., Nakamura S., Hazama T., Tashiro H., Itoh M., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yamamoto R., Matsumoto H., Sakaguchi S., Ikegami T., Kashiwagi K., Yoneda Y., Ishikawa T., Ozawa K., Tanaka T., Matsunia S., Kawai J., Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y., RIKEN integrated sequence analysis (RISA) system-384-format Genome Res. 10:1757-1771(2000).
                                                                                                        RIKEN FANTOM Consortium; "Functional annotation of a full-length mouse cDNA collection."; Nature 409:685-690(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 21.3%; Score 98; DB 2; Length 259; Best Local Similarity 36.1%; Pred. No. 0.0077; Matches 22; Conservative 5; Mismatches 30; Indels
                                                                   STRAIN=CS7BL/61; TISSUE=Head, and Whole body; MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28432 MW; E649ED8E3BC7E8E4 CRC64;
                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=CS7BL/6J; TISSUE=Head, and Whole body;
The FANTOM Consortium,
"High-efficiency full-length cDNA cloning.";
Meth. Enzymol. 303:19-44(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GO; GO:0005615; C:extracellular space; TAS.
InterPro; IPR066796; dickkopf N.
InterPro; IPR011052; Prot_amyI_inhib.
Pfam; PF04706; Dickkopf N; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                    SEQUENCE FROM N.A.
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67 C 67

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7 CDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCPCLPGLA

99

4; Gaps

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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
SUBMITTED (MAR-2004) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL, AYS75211, ASS915871, --
EMBL, AYS75211, ASS915871, --
EMBL, AYS75211, BAS915871, --
EMBL, AYS75211, --
EMBL, AYS752
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MEDLINE=20035735; PubMed=10570958; DOI=10.1016/S0378-1119(99)00365-0;
Krupnik V.E., Sharp J.D., Jiang C., Robison K., Chickering T.W.,
Amaravadi L., Brown D.E., Guyot D., Mays G., Leiby K., Chang B.,
Duong T., Goodearl A.D.J., Gearing D.P., Sokol S.Y., McCarthy S.A.;
"Functional and structural diversity of the human Dickkopf gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-UL-2004 (Rel. 44, Last annotation update)
Dickkopf related protein-2 precursor (Dkk-2) (Dickkopf-2) (hDkk-2)
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Oryctolagus cuniculus (Rabbit).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Lagomorpha, Leporidae, Oryctolagus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        amoo sapiems (Autanan).
Eukaryota, Metakona, Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
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Tanaka S., Sugimachi K., Sugimachi K.;
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
[3]
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77044F6D92C4014A CRC64;
                                                                                                                                                                                                                                                                    05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
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                                                                                                                                                                                                 268 AA
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268 AA; 28951 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23; Conservative
                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                      Dickkopf1 precursor.
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16-OCT-2001 (Rel
239
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Tanaka S., Sugimachi
Submitted (OCT-1999)
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Tate G., Mitsuya T.;
Submitted (NOV-1999)
sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                            SEQUENCE FROM N.A. TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI TaxID=9606;
                                                               NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     -i- TISSUB SPECIFICITY: Expressed in heart, brain, skeletal muscle and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        7 CDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCHPLTRKVPFFGRRMHHTCPCLPGLA
                  MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003; Clark H.P., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimconski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh V., Stinson J., Vagts A., Vandlen R., Watanabe C., Wieand D., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang Z., Goddard A., Wood W.I., Goddowski P., Gray A.,
                                                                                                                                                                                                                                                     "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins: a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lung.
-!- PTM: May be proteolytically processed by a furin-like protease.
-!- SIMILARITY: Belongs to the dickkopf family.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pfam; PF04706; Dickkopf_N; 1. _
Developmental protein; Glycoprotein; Signal; Wnt signaling pathway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   34 259 Dickkopf related protein-2.
78 127 DKK-type Cys-1.
183 256 DKK-type Cys-2.
52 N-linked (GlcNAc. . .) (Potential).
259 AA, 28447 MW, 39DDA3FA8975E87F CRC64;
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                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE OF 75-259 FROM N.A.

Tate G., Suzuki T., Mitsuya T.,
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
-i. FUNCTION: Inhibitor of Wnt signaling pathway (Potential).
-i. SUBCELLULAR LOCATION: Secreted.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.0%; Score 97; DB 1; Length 259; 36.1%; Pred. No. 0.0099; tive 5; Mismatches 30; Indels
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Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    171 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Potential.
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EMBL, AB035181; BAA87056.1; --
EMBL, AB035180; BAA87056.1; JOINED.
Genew; HGNC:2892; DKK2.
                                                                                                                                                                                                                                                                                                      bioinformatics assessment.";
Genome Res. 13:2265-2270(2003).
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ses 22; Conservative
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Matches
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52 CDNQRDCQPGLCCAFQRGL-LFPVCTPLPVEGELCHDPASKLLDLITWELEPDGALDRCP 110
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                                                                                                                                                                                         Ligon A.H., Pershouse M.A., Jasser S., Hong Y.K., Yung W.K.A., Steck P.A.;
Steck P.A.;
Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
EMBL, AR092661, C.extracellular; IEA.
GO; GO:0005275; P:development; IEA.
GO; GO:000178; P:negative regulation of Wnt receptor signali. ..; IEA.
InterPro; IPR00165; Prot and Inhib.
PF04706; Dickkopf N; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  7 CDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCH-PLTRKVPFFGRRMH-----HTCP
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MEDLINE=20035735; PubMed=10570958; DOI=10.1016/S0378-1119(99)00365-0;
Krupnik V.E., Sharp J.D., Jiang C., Robison K., Chickering T.W.,
Krupnik V.E., Sharp J.D., Mayd G., Leiby K., Chang B.,
Amaravadi L., Brown D.E., Guyot D., Mayd G., Leiby K., Chang B.,
Duong T., Goodearl A.D.J., Gearing D.P., Sokol S.Y., McCarthy S.A.;
"Functional and structural diversity of the human Dickkopf gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DKK3_HUMAN STANDARD; PRT; 350 AA.
Q9UBP4; Q9ULB7;
L6-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
25-JAN-2005 (Rel. 46, Last annotation update)
Dickkopf related protein-3 precursor (Dkk-3) (Dickkopf-3) (hDkk-3) (UNQ258/PRO295).
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20.6%; Score 95; DB 2; Length 171; 29.5%; Pred. No. 0.011;
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11; Mismatches 36; Indels
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to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF04706; Dickkopf N; 1. SEQUENCE 171 AA; 19283 MW; B890E38F873D0E62 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23; Conservative
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AB045206;
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Q8N294
     DORAN 
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Nausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Botachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Usdin T.B., Toobhyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
Broak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gay L.J., Hulyk S.W.,
Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Richards S., Worley K.C., Fale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Whiting M., Madan A., Young A. Scherkowko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
Broneration and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (see http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch)
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FUNCTION: Inhibitor of Wnt signaling pathway (Potential).
SUBCELLULAR LOCATION: Secreted.
TISSUE SPECIFICITY: Highest expression in heart, brain, and spinal
MEDLINE=21673998; PubMed=11814687; DOI=10.1016/S0378-1119(01)00838-1;
                                                                                                                                                                                                                                                                                                                          MEDLINE=22887296; PubMed=12975309; DOI=10.1101/gr.1293003; Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J., Chen J., Chow B., Crowley C., Currell B., Deuel B., Dowd P., Eaton D., Foster J., Grimaldi C., Gu Q., Hass P.E., Heldens S., Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J., Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J., Seshagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagts A., Vandlen R., Watanabe C., Meand D., Woods K., Xie M.-H., Yansura D., Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I., Godowski P., Gray A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The secreted protein discovery initiative (SPDI), a large-scale effort to identify novel human secreted and transmembrane proteins:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE OF 22-36.
PubMed=15340161; DOI=10.1110/ps.04682504;
Zhang Z., Henzel W.J.;
"Signal peptide prediction based on analysis of experimentally
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
                         Kobayashi K., Ouchida M., Tsuji T., Hanafusa H., Miyazaki M., Namba M., Shimizu N., Shimizu K.; Hanafusa H., Miyazaki M., "Reduced expression of the REIC/Dkk-3 gene by promoter-hypermethylation in human tumor cells."; Gene 282:151-158(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         bioinformatics assessment.";
Genome Res. 13:2265-2270(2003).
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AB033421; BAA85488.1; -. AB034203; BAA90548.1; -. AB035182; BAA87044.2; AB045205; BAA87044.2; JOINED.

EMBL;

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Dota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,

Makamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,

A Sekine M., Obayashi M., Nishi T., Shibahara T., Iahii S.,

Mamanoto J., Saito K., Kawai Y., Isono Y., Nakamura Y., Nagahari K.,

Murakami K., Yasuda T., Iwayanagi T., Wagatuma M., Shiratori A.,

A Sudo H., Hosoiri T., Kaku Y., Kodaira H., Kondo H., Sugawara M.,

Takahashi M., Kanda K., Yokoi T., Furuya T., Kikkawa E., Omura Y.,

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Ninomiya K., Ishibashi T., Yamashita H., Murakawa K., Fujimori K.,

A Tanai H., Kimata M., Watanabe M., Hiraoka S., Chiba Y., Ishida S.,

Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T., Kusano J.,

A Ranehori K., Takahashi-Fujii A., Hara H., Tanase T., Nomura Y.,

A Togiya S., Komai F., Hara R., Takeuchi K., Arita M., Imose N.,
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                              MIM; 605416; -.
GO; GO:0005615; C:extracellular space; TAS.
GO; GO:0005653; P:morphogenesis; TAS.
InterPro; IPR006796; dickkopf N.
InterPro; IPR011052; Prot amyl_inhib.
Pfam; PF04706; Dickkopf N.
Developmental protein; Direct protein sequencing; Glycoprotein; Signal; Wit signaling pathway.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            ..) (Potential)
..) (Potential)
..) (Potential)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 350;
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                                                                                                                                                                                                                                                                                                                                                                    protein-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         -> R (in Ref. 4).
72F504122B40AFFE CRC64;
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01-0CT-2002 (TrEMBLrel. 22, Last sequence update)
01-UNN-2003 (TrEMBLrel. 24, Last annotation update)
Hypotheital protein FLJ33633.
Homo sapiens (Human).
                                                                                                                                                                                                                                                                                                                                                                                                                        Poly-Ala.
N-linked (GlCNAC. .
N-linked (GlCNAC. .
N-linked (GlCNAC. .
N-linked (GlCNAC. .
G -> R (in Ref. 4).
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(GlcnAc.
(GlcnAc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; Score 95; DB 1;
; Pred. No. 0.022;
11; Mismatches 30
                                                                                                                                                                                                                                                                                                                                                                    related
                                                                                                                                                                                                                                                                                                                                                                Dickkopf related
DKK-type Cys-1.
DKK-type Cys-2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      215 AA.
, AB045207; BAA87044.2; JOINED.
, AB045208; BAA87044.2; JOINED.
, AB045209; BAA87044.2; JOINED.
, AB045210; BAA87044.2; JOINED.
, AB057591; BAB84360.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Amygdala;
PubMed=14702039; DOI=10.1038/ng1285;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CASGLLCQPHSHSLVYVC 284
                                                                                                               AY358378; AAQ88744.1; -.
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                                                     EMBL; AB045210; BAA87044.2; JG
EMBL; AB057591; BAB84360.1;
EMBL; AB057804; BAB84361.1;
EMBL; AX35378; AAQ88744.1;
EMBL; BC007660; AAH07660.1;
Genew; HGNC:2893; DKK3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38291 MW;
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350
195
284
343
343
106
121
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                                                                                                                                                                                            MIM; 605416; -
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                                                                                                                                                                                                                                                                                                                                                                                                      DOMAIN
DOMAIN
CARBOHYD
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CONFLICT
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              CARBOHYD
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email to license@isb-sib.ch)
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    or send an
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CARBOHYD
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Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
Moriya S., Momiyama H., Satoh N., Takami S., Terashima Y., Suzuki O.,
Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
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Pujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
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A Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.;
T. "Complete sequencing and characterization of 21,243 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9
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                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AK090952; BAC03555.1; -.
GO; GO:0005576; C:extracellular; IEA.
GO; GO:0007275; P:development; IEA.
GO; GO:0010718; P:nequative regulation of Wnt receptor signali. . .; IEA.
InterPro; IPR006796; dickkopf_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7 CDKDSQCGGGMCCAVSIWVKSIRICTPMGKLGDSCH-PLTRKVPFFGRRMH-----HTCP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-NOV-1997 (Rel. 35, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Dickkopf related protein-3 precursor (Dkk-3) (Dickkopf-3) (Lens fiber protein CLFEST4).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Archosauria, Aves, Neognathae, Galliformes, Phasianidae, Phasianinae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              20.5%; Score 94.5; DB 2; Length 215; 31.3%; Pred. No. 0.016; ive 8; Mismatches 31; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF04706; Dickkopf N; 1.
SEQUENCE 215 AA; 23904 MW; 2D9DEABCAFAE80B0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1997 (Rel. 35, Created)
                                                                                                                                                                                                                                                                                                                                                                                                     Genet. 36:40-45(2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CASGLLC 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 21; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 CLPGLAC 67
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090839;
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DKK3_CHICK
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              200 CENQHDCNPGTCCA---FQKELLFPVCTFLPEGGEPCHDPSNRLLNLITWELEPDGVLER 256
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MEDLINE=20500887; PubMed=11044603; DOI=10.1016/S0925-4773 (00) 00433-0; Shinya M., Eschbach C., Clark M., Lehrach H., Furntani Seiki M.; Schrach M., induced by the pre-MBT Wht signaling, is secreted from the prechordal plate and patterns the anterior neural plate."; mech. Dev. 98:3-17(2000).

EMBL, AF116852; AAD22461.1; EMBL, AF116852; AAD22461.1; Carls, 2DB-GENE-990708-5; dkkl.

ZFIN; 2DB-GENE-990708-5; dkkl.

GO; GO:000575; P:development; IEA.

GO; GO:0007275; P:development; IEA.

GO; GO:0007715; P:development; IEA.

GO; GO:0030178; P:negative regulation of Wnt receptor signali. ..; IEA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                     7 CDKDSQCGGGMCCAVSIWVKSI--RICTPMGKLGDSCH-PLTRKVPFFGRRMH-----HT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Brachydanio rerio (Zebrafish) (Danio rerio).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
Cyprinidae; Danio.
                                    InterPro; IPRO06796; dickkopf_N.
Pfam; PF04706; Dickkopf N; 1.
Developmental protein; Glycoprotein; Signal; Wnt signaling pathway.
SIGNAL
                                                                                                                                                                                                                                     (Potential). (Potential). (Potential).
                                                                                                                                                                                                                                                                                                                                                                                               11;
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                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 350;
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,0.041;
~heg 28; Indels
                                                                                                                           Dickkopf related protein-3.
                                                                                                                                                                                                                                                                                                       39208 MW; 57BE7ED850089DAE CRC64;
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                                                                                                                                             DKK-type Cys-1.
DKK-type Cys-1.
DKK-type Cys-2.
N-linked (GlCNAc...) (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                 9; Mismatches
                                                                                                                                                                                                                                                                                                                                               Score 92.5;
Pred. No. 0.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Created)
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SEQUENCE 241 AA; 26139 MW;
                                                                                                                                                                                                                                                                                                                                                      20.1%;
EMBL; D26311; BAA05373.1; -. HSSP; P25687; 11MT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TrEMBLrel. 12, (TrEMBLrel. 12,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best Local Similarity 36.1
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                   21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                          1113
196
282
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350
187
277
88
98
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 59 CPCLPGLAC 67
                                                                                                                                                                                                                                                                                                           350 AA;
                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=7955;
                                                                                                                                30
1139
200
88
98
1113
1196
282
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SEQUENCE FROM N.A.
STRAIN=C57BL/6J; TISSUB=Liver;
MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Cloning, expression, and functional characterization of the substrate binding subunit of rat type II iodothyronine 5'-deiodinase."; J. BIOL. Chem. 275:25194-25201(2000).

EMBL; AF245040; AAG15890.1; -
GO; GO:0005576; C:extracellular; IEA.
GO; GO:000775; P:development; IEA.
GO; GO:00030178; P:negative regulation of Wnt receptor signali. . .; IEA.
InterPro; IRR066796; dickkopf_N.
Fram; PF04706; Dickkopf_N; BO:0570676; GO:0570676; GO:05
                                                                                                                                           01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
Substrate binding subunit of type II 5'-deiodinase D2p29.
Rattus norvegicus (Rat).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
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MEDLINE-20035735; Pubmed-10570958; DOI=10.1016/S0378-1119(99)00365-0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=Sprague-Dawley; TISSUE=Brain;
MEDLINE=20460444; PubMed=10829019; DOI=10.1074/jbc.M002036200;
Leonard D.M., Stachelek S.J., Safran M., Farwell A.P., Kowalik T.F.,
Leonard J.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Krupnik V.E., Sharp J.D., Jiang C., Robison K., Chickering T.W., Amaravadi L., Brown D.E., Guyot D., Mays G., Leiby K., Chang B., Dhong T., Goodearl A.D.J., Gearing D.P., Sokol S.Y., McCarthy S.A., "Functional and structural diversity of the human Dickkopf gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Dickkopf related protein-3 precursor (Dkk-3) (Dickkopf-3) (mDkk-3)
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Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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9; Mismatches 31; Indels
                                                                                      277 AA.
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                                                                                      PRELIMINARY;
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Gene 238:301-313(1999).
[3]
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Matches
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RA Medide I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., RA Mikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H., RA Yagi K., Tomatu Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T., Baldarelli R., Halil D.P., Bult C., Hume D.A., Quackenbush J., Schrim I.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W., Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J., Schrim I.M., Kanapin A., Matsuda H., Fatalov S., Beisel K.W., Balke J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., RA Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S., RA Garimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., RA Garimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D., RA Amai A., Kawaji H., Kawasawa Y., Kedzierski R.W., King B.L., Kawaji H., Kawasawa Y., Kedzierski R.W., Fungaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A., Ranai A., Kawaji R., Pontius J.U., Di D., Ramachandran S., Ranachandran S., Jarvis E.D., RA Nagashima T., Numata K., Okido T., Pavan W.J., Parta G., Ringwald M., Pallai R., Pontius J.U., Oi D., Ramachandran S., Ashalelia R., Schneider C., Serou M., Shimada K., Angule C.A., Serou M., Shimada K., Angule C.A., Serou M., Shimada K., Angule C.A., Serou M., Yang I., Yang I., Yang I., Yang I., Wannar B., Wanner E., Wahlestedt C., Wang Y., Watanabe Y., Walls C., Wanna Y., Watanabe Y., Walls C., Wanna Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatawa I., Rahixume W., Independent K., Baitaki Y., Kawai J., Aizawa K., Arakawa T., Fukuda S., Ranaki D., Shibata K., Shinagawa H., Barnaki Y., Shinaga A., Baitaki Y., Sasaki D., Shibata K., Shinaga A., Ranakaki Y., Sasaki D., Shibata K., Shinaga A., Ranakaki Y., Ranalyaisi Gf the mouse transcriptome based on functional annotation of K. Indure 420:563-573(2002).
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SEQUENCE FROM N.A.

SEQUENCE TSSUE=Brain, and Retina;

STAIN=C37BL/6; TISSUE=Brain, and Retina;

RADIND=223B8257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RADIND=223B8257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Alteschul S.F., Zeeberg B.A. Retow K.H., Schaefer C.F., Bhat N.K.,

RA Alteschul S.F., Jordan H., Moore T., Max S.I., Wang J., Heiseh F.,

RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M.J., Usdin T.B. Ronaldo M.F., Caarninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Rownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

RA Rochards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Whiting M., Madan A., Young A.C., Shevchenko Y. Bouffard G.G.,

Whiting M., Adan A., Young A.C., Shevchenko Y. Bouffard G.G.,

RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,

RY "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences ";

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

Proc. ITSSUE SPECIFICITY: Highest expression in brain, eye and heart.

C. -: FUNCTION : Linishest capte expression in brain, eye and heart.
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EMBL, FAT77400; AAF02680.1; -.
EMBL, AK004853; BAB23617.1; -.
EMBL, BC046304; AAH46304.1; -.
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EMBL; BCO50934; AAH50934.1; -.
MGD; MGI:1354952; Dkk3.
MICLEPPO; IPRO0679; dickkopf_N.
Pfam; PPO4706; Dickkopf_N; 1.
Developmental protein; Glycoprotein; Signal; Wnt signaling pathway.
                                                                                                               Potential.

Dickkopf related protein-3.

DKK-type Cys-1.

DKK-type Cys-2.

N-linked (GlCNAC. .) (Potential).

N-linked (GlCNAC. .) (Potential).

N-linked (GlCNAC. .) (Potential).
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Nature 391:357-362(1998).

EMBL, AF030434; AAC02427.1; -.

EGO; GO:0005576; C:extracellular; IEA.

GO; GO:0007275; P:development; IEA.

GO; GO:0030178; P:negative regulation of Wnt receptor signali...

InterPro; IPR006796; dickkopf_N.
                                                                                                                                                                                                                                                                                                                                                     19.6%; Score 90.5; DB 1; Length 349; 29.9%; Pred. No. 0.069; ive 9; Mismatches 31; Indels 7
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                                                                                                                                                                                                                                                                                            - Linkea (Gichac. . .) (Po
564CB3C4FB2EAB88 CRC64;
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Last sequence update)
Last annotation update)
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259 AA; 28865 MW;
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Signal.
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Matches 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 29.9 Matches 20; Conservative
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195
284
96
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                                                                                                                                                                                                                                                                                                             349 AA;
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Name=Xdkk-1;
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CARBOHYD
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Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
                                                                                                                                                                                                                                                                                                                                                TISSUE-Liver;
Hsieh S.-Y., Hsieh P.-S., Chen W.-Y.;
Submitted (APR-2004) to the EMBL/GenBank/DDBJ databases.
EMBL; AYS67550; AAS6757.1; -.
GO, GO:0005576; C:extracellular; IEA.
GO, GO:0007275; P:development; IEA.
GO, GO:0030175; P:negative regulation of Wnt receptor signali.
InterPro; IPR006796; dickkopf_N.
ERGUENCE 350 AA; 38340 MW; E88BBSC3FB294D41 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   .;
8
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19.3%; Score 89; DB 2; Length 350;
Best Local Similarity 28.2%; Pred. No. 0.1;
Matches 22; Conservative 11; Mismatches 37; Indels
                                                                        05-JUL-2004 (TrEMBLrel. 27, Last sequence update) 05-JUL-2004 (TrEMBLrel. 27, Last annotation update) Putative tumor suppressor Dkk-3/REIC.
350 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           completed: November 7, 2005, 21:00:03
                                                       Created)
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                           06P081;
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
05-JUL-2004 (TrEMBLrel. 27,
     PRELIMINARY;
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                                                                                                                                                                 Name=DKK3;
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